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UG-08-981-192-2

Sequence 2, Application US/Uo.
Sequence 2, Application US/Uo.
Sequence 2, Application US/Uo.
Sequence 2, Application US/Uo.
Sequence 3, Application US/Uo.
SepticANT: Henrique, Domingoe Manuel Pinto
APPLICANT: Lewis, Julian Hart
APPLICANT: Lewis, Julian Hart
APPLICANT: Gray, Grace
TITLE OF INVENTION: WOLCEOTIDE AND PROTEIN SEQUENCES
TITLE OF INVENTION: WOLCEOTIDE AND PROTEIN SEQUENCES
TITLE OF INVENTION: OF VERTERATE DELTA GENES AND WETHODE BASED
ORNERSONDENCE ADDRESS:
ADDRESSES: Pennie & Edmonds Lip
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NU
COUNTRY: USA
ZIP: 10056/271

COMPUTER FEBALALE TORN:
MEDILUTYPE: Diskette
COMPUTER FEBALALE
COMPUTER FEBALALE
COMPUTER FEBALALE
MEDILUTY APPLICATION DOS
SOCTAARS: TRECOMPUTER: 1806/981.392
FILLING DATE: 22-DEC-1997
FILLING DATE: 22
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US-08-981-392-6
US-08-908-322-6
US-08-400-159-6
US-08-400-159-6
US-09-917-254-85
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Mismatches
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Pred. No. 1
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,3:
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                               APPLICATION NUMBER: 08/981,39:
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                        LENGTH: 728 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown;
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID N(US-09-908-322-2)
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Best Local Similarity 100.0%;
Matches 728; Conservative
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AND METHODS BASED
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LI
STREET: 1155 Avenue of the Ame
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VT: Ish-Horowicz, David
Henrique, Domingos Ma
Lewis, Julian Hart
Artavanis-Tsakonas, S
Gray, Grace
F INVENTION: NUCLEOTIDE A
VERTEBRATE D
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Sequence 2, Application Userient No. 6783956
GENERAL INFORMATION:
APPLICANT: ISh-Hore
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SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,392
FILING DATE: 22-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                         RESULT 3
US-08-872-855-8
; Sequence 8, Application US/08872855
; Patent No. 6121045
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean
; APPLICANT: Gearing, David
; TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
; TITLE OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,855 ~> 08/632/
FILING DATE: 11-JUN-1997
CLASSIFICATION: 514
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Pred. No. 6.5e-304;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                    3: FOLEY, HOAG & ELIOT LLP
One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
   TELEPHONE: 617-832-1000
   TELEFAX: 617-832-7000
   INFORMATION FOR SEQ ID NO: 8:
   SEQUENCE CHARACTERISTICS:
   LENGTH: 729 amino acids
   TYPE: amino acid
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ilarity 99.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,
REFERENCE/DOCKET NUMBER:
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Matches 728; Conser
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TOPOLOGY: 1
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RESULT 4

US-08-981-392-5

; Sequence 5, Application US/08981392

; Patent No. 6262025

; GENERAL INFORMATION:

; APPLICANT: Henrique, Domingos Manuel Pinto

APPLICANT: Henrique, Domingos Manuel Pinto

; APPLICANT: Artavanis-Tsakonas, Spyridon

; APPLICANT: Artavanis-Tsakonas, Spyridon

APPLICANT: Artavanis-Tsakonas, Spyridon

; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES

; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON

; NUMBER OF SEQUENCES: 94

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

CITY: New York

; STATE: NY
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                                                   HGFCDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCT
                                                                                                                     HHKPCKNGATCTNTGQGSYTCSCRPGYTGSSCEIEINECDANPCKNGGSCTDLENSYSCT
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                                                                   721
                                                                   Length
                                                                             Indels
                                                                  ore 3495.5; DB 3 ed. No. 3.7e-255; Mismatches 54;
                                                                   Score Pred.
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-790-9090
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 amino acids
TYPE: amino acids
                                                                             65;
                                                                  / Match
Local Similarity 82.2%;
nes 600; Conservative
                                  TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-981-392-5
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RESULT 5 US-09-908-322-5 ; Sequence 5, Application US/09908322

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                                                                                    N SEQUENCES OF
AND METHODS BASED
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Pred. No. 3.7e-255;
5; Mismatches 54;
                                                                                    AND PROTEIN DELTA GENE 1
                                                             Spyridon
                                                                                                                                                                                                                                                                                            , 322
                                                                                                                                                                                                                                                                                                                                                                                                           7326-123
                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,32;
FILING DATE: 17-Jul-2001
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S Leslie
REGISTRATION NUMBER: 18,872
                                      Manuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 732(
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 ----
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N
                                  Henrique, Domingos Ma
Lewis, Julian Hart
Artavanis-Tsakonas, S
Gray, Grace
? INVENTION: NUCLEOTIDE A
VERTEBRATE D
                        David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 721 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: <Unknown>
                                                                                                                                                                                                 ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65;
                                                                                                         NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & EG
STREET: 1155 Avenue o
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illarity 82.2%;
Conservative 6
                        Ish-Horowicz
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                                                                                                                                                               New York
6783956
INFORMATION
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                                                                                                                                                                                         COUNTRY:
ZIP: 1003
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                        APPLICANT:
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HGFCDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCT
                                                           NGKNÇSTPVSRCEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDFT
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Pred. No. 4.4e-255;
; Mismatches 64;
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US-09-423-753-27
US-09-423-753-27

Sequence 27, Application US/09423753

Patent No. 6664098

GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL DIFFERENTIATION INF
FILE REFERENCE: KP-8693

CURRENT APPLICATION NUMBER: US/09/423,753

CURRENT FILING DATE: 1999-12-30

PRIOR PPLICATION NUMBER: PCT/JP98/02104

PRIOR APPLICATION NUMBER: JP 9/124064

PRIOR FILING DATE: 1997-05-14

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 27

LENGTH: 723
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Best Local Similarity 83.3%;
Matches 609; Conservative
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                                                                                                                                                                                                                                                                                  Sequence 9, Application US/09068740A
; Sequence 9, Application US/09068740A
; Patent No. 6337387
; GENERAL INFORMATION:
; APPLICANT: SAKANO, SEIJI
APPLICANT: ITOH, AKIRA
; TITLE OF INVENTION:
; FILE REFERENCE: KP-8447
; CURRENT APPLICATION NUMBER: US/09/068,740A
; CURRENT FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: JP 7-29611
; PRIOR APPLICATION NUMBER: JP 7-311811
; PRIOR APPLICATION NUMBER: PT 7-311811
; PRIOR FILING DATE: 1995-11-17
; PRIOR FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIN Ver. 2.1
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Pred. No. 4.4e-255;
47; Mismatches 64;
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illarity 83.3%;
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Best Local Similarity
Matches 609; Conser
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JS-08-872-855-7
Sequence 7, Application US
Patent No. 6121045
GENERAL INFORMATION:
APPLICANT: McCarthy, S
APPLICANT: Gearing, Da
TITLE OF INVENTION: NC
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-346
Prior Application NUMBER OF SEQ ISEQ ID NO 346
LENGTH: 723
TYPE: PRT
ORGANISM: Homo
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          SVKEEHGKCEAKCETYDSEAEEK-SAVOLKSSDTSERKRPDSVYSTSKDTKYQS
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Sequence 346, Application US/10140002

Patent No. 6725730

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: Beresini, Maureen

APPLICANT: Beresini, Maureen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gao, Wei-Qiang

APPLICANT: Godowski, Paul J.

APPLICANT: Godowski, Paul J.

APPLICANT: Sherwood, Steven

APPLICANT: Sherwood, Steven

APPLICANT: Stewart, Timothy A.

APPLICANT: Stewart, Timothy A.

APPLICANT: Watanabe, Colin K

APPLICANT: Wata
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  THEREFOR
                                                                                                                Version
                                                                                                                                                                   NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MAA-003.02
                                STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
  USES
                           LLP
                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,85!
FILING DATE: 11-JUN-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: THERAPEUTIC UNUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT
STREET: One Post Office Square
                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 721 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 599; Conser
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TOPOLOGY: lii
MOLECULE TYPE:
S-08-872-855-7
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SYRFVCDEHYYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDEQ
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                                                                                                                                                                                                        AND
                                                                                                                                                         US-09-641-612-6

Sequence 6, Application US/09641612

Patent No. 6703221

GENERAL INFORMATION:

APPLICANT: Vivien Chan et al.

TITLE OF INVENTION: NOTCH RECEPTOR LIGANDS AN

FILE REFERENCE: PPO-1602.002 / 200130.498

CURRENT APPLICATION NUMBER: US/09/641,612

CURRENT FILING DATE: 2000-08-17

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                47;
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Best Local Similarity 82.8%;
Matches 605; Conservative
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 NGGRCTDNPDGGYSCRCPLGYSGFNCEKKIDYCSSSPCANGAQCVDLGNSYICQCQAGFT
              HERSNRYVCECARGYGGLNCOFLLPEPPOGPVIVDFTEKYTEGONSOFPWIAVCAGIILV
                                                                                                            LMLLLGCAAIVVCVRLKVQKRHHQPEACRSETETMNNLANCQREKDISISVIGATQIKNT
                                                                                                                                                                                                NKKVDFHSDNS-DKNGYKVRYPSVDYNLVHBLKNED-SVKEEHGKCEAKCETYDSEAEEK
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; Patent No. 6121045
; Patent No. 6121045
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean
; APPLICANT: Gearing, David
; TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
; TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
; CITY: Boston
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Pred. No. 4.4e-246
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Mismatches
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FR: MAA-003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/872,85: FILING DATE: 11-JUN-1997 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: UZIUZ-LI
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MAA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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ilarity 79.2%;
Conservative 7:
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Best Local Similarity
Matches 579; Conser
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US-08-872-855-4
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TYPE: a
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STATE:
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                                    TYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFGFTWPGTFSLIIEALHTDSPDDLT
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Sequence 4, Application US/09068740A

GENERAL INFORMATION:

APPLICANT: SAKANO, SEIJI

TITLE OF INVENTION:

FILE REFERENCE: KP-8447

CURRENT APPLICATION NUMBER: US/09/068,740A

CURRENT FILING DATE: 1998-06-18

PRIOR APPLICATION NUMBER: JP 7-299611

PRIOR APPLICATION NUMBER: JP 7-299611

PRIOR FILING DATE: 1995-11-17

PRIOR FILING DATE: 1995-11-30

PRIOR FILING DATE: 1995-11-30

PRIOR FILING DATE: 1996-11-15

NUMBER OF SEQ ID NOS: 48

SOFTWARE: PatentIN Ver. 2.1
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larity 84.0%; Pred. No. 2.1e-251;
Conservative 46; Mismatches 58;
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713 EKDECVIATEV 723
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Best Local Similarity
Matches 595; Conser
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LENGTH: 702
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les 72;
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Pred. No. 1.5e
3; Mismatches
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                                 39
                                                                              -03
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,35
FILING DATE: 22-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 722 amino acids
TYPE: amino acid
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                                                                                                                                                                                   81.1%;
ilarity 78.5%;
Conservative 7:
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                                                                                                                                                       unknown
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: Local Similarity
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TOPOLOGY: u
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  MGRRSALALAVVSALL - - CQVWSSGVFELKLQEFVNKKGLLGNRNCCRGGSGP
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Sequence 12, Application US/08981392
Patent No. 6262025
GENERAL INFORMATION:
APPLICANT: Ish-Horowicz, David
APPLICANT: Henrique, Domingos Manuel Pinto
APPLICANT: Lewis, Julian Hart
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Gray, Grace
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASE
NUMBER OF SEQUENCES: 94
                                                                          the America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEE: Pennie & Edmonds LLP: 1155 Avenue of the Amer: New York
                                                                                                                                                                                                                                                                                                                                                       728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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CITY: Ne
STATE: N
COUNTRY:
ZIP: 100
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REFERENCE/DOCKET NUMBER: MAA-003.02
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,855
FILING DATE: 11-JUN-1997
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; Sequence 5, Application US/08872855
; Patent No. 6121045
; Patent No. 6121045
; GENERAL INFORMATION:
    APPLICANT: McCarthy, Sean
    APPLICANT: Gearing, David
    TITLE OF INVENTION: THERAPEUTIC US:
    NUMBER OF SEQUENCES: 23
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: FOLEY, HOAG & ELIOT LL
    STREET: One Post Office Square
    CITY: Boston
    STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
TTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,
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INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
VERTEBRATE DELTA GENE AND METHODS BASED
atvrdthskrdtkcqsqslqekrspqhlgvgrfltenrpesvystskdtkyqs
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larity 78.5%; Pred. No. 1.5e-245;
Conservative 73; Mismatches 72;
                                                                                                                                                                            Manuel Pinto
                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                              Edmonds LLP
of the Americas
                                                                                                                                                                                                    Spyridon
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                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                             APPLICANT: Ish-Horowicz, David
Henrique, Domingos Menrique, Julian Hart
Artavanis-Tsakonas,
                                                                                                            5-09-908-322-12
Sequence 12, Application US/09908322
Patent No. 6783956
GENERAL INFORMATION:
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
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ADDRESSEE: Pennie &
STREET: 1155 Avenue
CITY: New York
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                                                              Score 3346.5; DB 3
Pred. No. 6.2e-244;
; Mismatches 69;
                                                                         67;
; TELEFAX: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
; LENGTH: 713 amino acids
; TYPE: amino acid
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-872-855-5
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                                                              Query Match
Best Local Similarity 78.5%;
Matches 574; Conservative
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Compugen Ltd.
GenCore version (c) 1993 - 2004
          Copyright
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model **8**% using - protein search, OM protein

Seconds ; Search time 76.5563 (without alignments) 3411.281 Million cell 13:11:34 2004, November 29, Run on:

updates/sec

US-09-783-931-2 4153 1 MGGRFLLTLALLSALLCRCQ......xQSVYVISEEKDECIIATEV Title: Perfect score: Sequence:

728

Gapext BLOSUM62 Gapop 10.0 Scoring table:

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2002273 of hits satisfying chosen parameters: Total number

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A Geneseq 23Sep04:*

1: geneseqp1980s:*

2: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description			79029 Chick	18353 Prolifer	2 Human d	8 Human de	83227 PRO172	33422 Human PR	24388 Human P	00172 PRO172	12344 Human PR	53064 Huma	7788 Novel	104	66742 Huma	59	501	67018 Human	Ada45865 Novel hum	76296	189	1569 Ношо в	354 Novel	Adb27895 Human PRO	374
SUMMARIES		Π	AW0087	AAW11719	AAY79029				22				1234	5306	778	104	674	ABU59823	501	6701		29	1894	9519	35	2789	
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ALIGNMENTS

lung cancer;		
) otein; 740 AA. ntry) (alternatively spliced variant). feration; nervous system disorder; Notch; cervix cancer; breast cancer; s; seminoma; neurogenesis; therapy.	Location/Qualifiers	/label= EGF8 524534 /label= EGF9 555579 /label= TM /note= "transmembrane domain" 96WO-US011178.
0087 0087 APR- elte elte sue on c	Key Domain Domain Domain Domain Domain Domain Domain Domain Domain Domain	571-A1. -1997. -1996;
RESULT 1 AAW00876 ID AAW XX AC AAW XX DT 28- XX C-D XX KW C-D XX KW C-D XX XX	XEELELEEEEEEEEE	FFFFFXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

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New vertebrate Delta protein, DNA and antibodies - for treating and preventing cancer, nervous system disorders and for tissue regeneration.
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tissue regeneration; Notch; cervix cancer; breast cancer;
colon cancer; melanoma; seminoma; neurogenesis; therapy.
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184. .228
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229. .261
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/label= EGF2
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/label= EGF3
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555. .579
/label= TM
/note= "trans
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/label= EGF1
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N-PSDB; AAT58897.
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Gray GE;
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                                                                                                                                                C-delta-1 polypeptide (AAW00876) is the chick homologue of Drosophila Delta, a protein that binds to Notch protein. Expression of C-Delta-1 correlates with onset of neurogenesis. The C-delta-1 amino acid sequence was deduced from a cDNA clone (AAT58898) obtd. from chick stage 4-6 embryos. A shorter version (AAW58877) of C-Delta-1, lacking the 12 C-terminal amino acids of the longer version, was also isolated, and mouse (AAW11720) and human (AAW11721-38) Delta-1 polypeptides have been identified. Delta-1 proteins can be used to treat or prevent disorders characterised by increased Notch activity, such as cervical, breast, lung or colon cancer, melanoma or seminoma, and nervous system disorders or to promote tissue regeneration and repair
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Pred. No. 7.2e-228;
Mismatches 0;
                                                                                                    and antibodies
disorders and
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                                          Lewis
                                                                                                    New vertebrate Delta protein, DNA preventing cancer, nervous system
                                                                                                                                  English
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Best Local Similarity 100.0%;
Matches 728; Conservative (
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            CANCER RES
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                                                                                                                                 Disclosure; Fig 2; 135pp;
                                                                       WPI; 1997-100159/09
N-PSDB; AAT58898.
                                                                                                             preventing cancer,
           IMPERIAL CUNIV YALE.
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                                        Ish-Horowicz
Gray GE;
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                                                                  Delta, a protein that binds to Notch protein. Expression of C-Delta-1 correlates with onset of neurogenesis. The C-delta-1 amino acid sequence was deduced from a cDNA clone (AAT58897) obtd. from chick stage 4-6 embryos. An alternatively spliced variant (AAW00876) was also isolated, and mouse (AAW11720) and human (AAW11721-38) Delta-1 polypeptides have been identified. Delta-1 proteins can be used to treat or prevent disorders characterised by increased Notch activity, such as cervical, breast, lung or colon cancer, melanoma or seminoma, and nervous system disorders or to promote tissue regeneration and repair
                                                      Drosophila
f C-Delta-1
                                                        chick homologue
                                                       the
                                                      <u>i</u> 8
                 English
                                                       (AAW11719)
                 135pp;
                                                       polypeptide
                 7
                Fig
                 Disclosure;
                                                     C-delta-1
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Sequence 727 AA;

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                                             CKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFG
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            Indels
Score 4119.5; DB 2;
Pred. No. 5.7e-226;
); Mismatches 2;
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Local Similarity 99.6%;
les 725; Conservative
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Delta, Kuz, Notch, differentiation, cervical, breast, colon, cancer, lung, melanoma, seminoma, central nervous system disorder, psoriasis tissue regeneration, liver cirrhosis, keloid formation, baldness, inner ear disorder, chick.
                                           acid sequence
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                                                                                                                                                        Rand MD,
                                                                                                                             98US-0092513P
98US-0104834P
                                                                                                                  99WO-US015817
          standard; protein;
                                           amino
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                                           delta protein
                               (first
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                                                                                                                                              (UYYA ) UNIV YALE
                                                                                            WO200002897-A2
                                06-JUN-2000
                                                                                                       0-JAN-2000
                                                                                                                             13-JUL-1998
19-OCT-1998
                                                                                                                  13-JUL-1999
                                                                                  Gallus sp.
                    AAY79029;
          AAY79029
                                          Chick
RESULT 3
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New cleavage peptide, nucleic acids and antibodies useful for diagnosis, prevention and treatment of cancer, disorders of central nervous system, cirrhosis and psoriasis

Claim 1; Fig 3; 177pp; English.

This sequence represents the chick delta protein amino acid sequence.

Delta is a toporythmic protein that contains a sequence which is cleaved by the metalloprotease-distintigrin (Kuzbanian (Kuz). Cleavage by Kuz results in two fragments, a soluble amino terminal fragment consisting essentially of the extracellular domain, and a membrane bound fragment consisting essentially of the extracellular domain, and a membrane bound fragment consisting essentially of the extracellular domain. The consisting of the transmembrane domain and the intreactallular domain. The soluble fragment is able to bind to Notch. Delta plays a key role in differentiation, and therefore detection and measurement of delta activation is important in the study of differentiation. The invention relates to the delta cleavage peptides (the activation belta cleavage peptides to methods for detecting and measuring delta activation. Delta cleavage peptides of methods for detecting and measuring delta activation. Delta cleavage peptides or an clear protein are useful for medulating the activity of modulated and vice versa. A delta cleavage peptide or its derivative capable of binding kuz protein is useful for treating or preventing a disease or disorder associated with increased delta activity or expression such as cervical, breast, colon or lung cancer, melanoma or seminoma in humans. A recombinant cell comprising a delta peptide is useful for the diagnosis of diseases or disorders associated with increased levels of Nocch-delta protein bind kuz protein. A complex, colon or lung cancer, melanoma activity comprising measuring the ability of delta cleavage peptide is useful for the diagnosis of diseases or disorders associated with aberrant levels of the complex, comprising measuring the ability of delta cleavage peptide is useful for the presence of, or predisposition to complex, comprising measuring the ability of delta cleavage peptide is associated with aberrant levels of complex, complex, complex, complex, keloid formation, psortsais, baldness

Sequence 728 AA;

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HGFCDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCT
                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a polypeptide which suppresses proliferation and differentiation of undifferentiated cells such as neurons and blood cells. The polypeptide may be used for the prevention and control of disorders involving undifferentiated cells, such as leukaemia and malignant tumours, and improvement of blood formation, after immunosuppression
                                                                                                                                                                                                                                                                                                  NGKNCSTPVSRCEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDFT
                                                                                                                                      delta-1 and serrate-1 - suppress of undifferentiated human blood
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                         suppression_protein
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Pred. No. 1.8e-190;
17; Mismatches 64;
Location/Qualifiers
1. .21
/label= Signal
22. .723
/label= Differentiation_s
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                                                                                                                                      by human genes
differentiation
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                                                              96WO-JP003356
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95JP-00311811
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Best Local Similarity 83.3%;
Matches 609; Conservative
                                                                                            KOGYO
                                                                                                                                                         Claim 15; Page 77-82;
                                                                                            KASEI
                                                                                                                    1997-298110/27
                                                                                                                                      Peptide(s) encoded proliferation and
                                                                                                        Itoh A;
                                                                                                                          AAT70174
                                                                                                                                                                                                               Sequence 723 AA;
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                                     WO9719172-A1
                                                                         17-NOV-1995
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neuron; leukaemia; r
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       Query Match
Best Local Similarity 99.0%;
Matches 721; Conservative
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                                            proliferation;
  MGSRCALALAVLSALL--CQVWSSGVFELKLQEFVNKKGLLGNRNCCR-
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22. .723
/label= Delta-1
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leukaemia; malignant tumour
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                                                                                                                                                                                                                             cell; pri
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Pred. No. 1.8e-190;
7; Mismatches 64;
                                                                                                                                                                                                                                                                                               delta-1 protein"
                                                                                                                                                                                                                                                                                 peptide"
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83.3%;
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22...7
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N-PSDB; AAX16817.
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Best Local Similarity
Matches 609; Conser
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amplification.
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Inhibition; cancer; neoplasia; tumour; breast; ovary; renal; colorectal; uterus; prostate; lung; bladder; central nervous system; CNS; melanoma; leukaemia; PRO211; PRO228; PRO538; PRO172; PRO182; human.
/note= "Casein kinase II phosphorylation site"
243. .255
/label= EGF-like_domain
252. .261
/note= "Tyrosine kinase phosphorylation site"
262. .268
/note= "N-myristoylation site"
274. .286
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/note= "Casein kinase II phosphorylation sit 154. .158
/note= "Casein kinase II phosphorylation"
176. .185
/note= "Tyrosine kinase phosphorylation site 203. .207
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"3. .97

/note= "Casein kinase II p.

98. .104

/note= "N-myristoyl"

99. .105

/note= "N-m."
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/note= "EGF-like domain"
281. .287
/note= "N-myristoylation s
282. .288
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/label= Signal_peptide
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301. .307
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Pred. No. 1.8e-190;
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ilarity 83.3%;
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N-PSDB; AAX16300
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            9-NOV-1998
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548. .568
/label= Transmembrane_domain
552. .563
/label= Prokaryotic membrane lipoprotein lipid
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659. .663
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/label= Asn and Asp hydroxylation site
167. 479
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/note= "N-glycosylation site"
483. .487
/note= "Casein kinase II phosphorylation site"
495. .499
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660. .664
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/label= EGF-like_domain
169. .373
/note= "Casein kinase II
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note= "Casein kinase II
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phosphorylation site"
670. .674
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342. .3
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                                         Composition for inhibiting neoplastic cell growth and treating cancers ovary, uterus, prostate, lung and bladder, comprises PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptide or their agonist.
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                                                                           Compositions comprising a PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptide or their agonists, mixed with a carrier is useful for inhibiting neoplastic growth and treating tumors such as cancers of breast, ovary, renal, colorectal, uterus, prostate, lung, bladder, central nervous system, melanoma and leukaemia
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N-PSDB; AAZ93703.
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Human; immune related disease; diagnosis; antiinflammatory; cardiant;

Mermatological; antiarthritic; antirheumatic; immunosuppressive;

Maemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;

Mantianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;

Mantiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;

Mantiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;

Maliopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;

Maliopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;

Maliomanne thrombocytopaenia; immune-mediated renal disease;

Maliomantory bowel disease; gluten-sensitive enteropathy;

Maliomanne disease; immune-mediated skin disease; allergic disease;

Mimmunological disease; transplantation associated disease;

Maraft rejection; graft-versus-host-disease.
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99US-0123618P.
99US-0123957P.
99US-0125775P.
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99US-0131445P.
99US-01312371P.
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The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, overlanding architis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases of the central and peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases, allergic diseases, immunological disease, peripheral nand graft-versus-host-diseases. AACS83878 cepresent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AACS879 to AACS8578 cepresent human PRO polynucleotide and protein sequences given in the ceremplification of the present invention
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Wood WI, Yan M;
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an J, Pennica
Watanabe CK,
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2000WO-US004342.
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Matches 609; Conservative
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Lu Y, Pan
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diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic,
cytostatic; gene therapy; vaccine.
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AAB24388 standard; protein; 723
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99US-0131445P.

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99WS-0134287P.

99WS-0141037P.

99WO-US012252.

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Smith V, Watanabe CK,
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08-MAR-1999;
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28-APR-1999;
02-JUN-1999;
23-JUN-1999;
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The present invention describes nucleic acids encoding PRO polypeptides
useful for preventing, diagnosing and treating diagnosing a
cardiovascular, endothelial or angiogenic disorder in mammals by
modulating cell proliferation, angiogenesis and cardiovascularisation,
and for identifying agonists and antagonists of these processes. The
reatment and diagnosis of diseases associated with inappropriate PRO
expression such as cardiovascular, endothelial or angiogenic disorders in
mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For
example, the nucleic acids (NCs) and vectors containing them and the PRO
polypeptide may be used to treat disorders associated with decreased PRO
expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent
nucleotide and protein sequences used in the exemplification of the
s encoding PRO polypeptides useful for preventing, diagnosing diagnosing a cardiovascular, endothelial or angiogenic mammals.
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                                                                                                                                         Isolated PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptides or their agonists (preferably anti-PRO agonist antibody or a small molecule mimicking the biological activity of PRO polypeptide) are useful in vitro or in vivo for inhibiting the growth of a tumour cell. Compositions comprising the PRO polypeptides are useful for inhibiting neoplastic cell growth and for treating cancer including breast, ovarian, renal, cancer, melanoma and leukaemia in a mammal. The PRO polypeptides are also useful for treating other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal, blastocoelic disorders and inflammatory, angiogenic and immunologic disorders as well as being useful for identifying agonists to PRO polypeptides by contacting the polypeptide with a candidate molecule and conitoring biological activity mediated by the polypeptide
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                                                                                                                                                                                                                                     AAU12172-AAU1246 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation of proteoglycans from cartilage, the printer ear utricular supporting cells or of T-prophocytes, the release of proteoglycans from cartilage, the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polymucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy
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PJ, Gurney
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Pred. No. 1.8e-190;
47; Mismatches 64;
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A, Godowski I
Tumas D, Wata
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2000WO-US020710.
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2000WO-US023522.
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art TA,
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Best Local Similarity
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                                                                                                      Gerritsen ME,
Smith V, Stev
28-JUL-2000;
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23-AUG-2000;
24-AUG-2000;
08-NOV-2000;
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                                                                                            CTCPPGY
                                                                                                                                             Human; angiogenesis-associated protein; PRO; endothelial cell growth cardiac hypertrophy; cardiovascular disorder; endothelial disorder; angiogenic disorder; atherosclerosis; osteoporosis; hypertension; myocardial infarction; diabetic retinopathy; rheumatoid arthritis; Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; can Alzheimer's disease; Huntington's disease; stroke; drug screening; gene therapy; transgenic animal.
                                                             CANGAQCVDLGNSYICQCQAGFTGRHCDDNVDDCASFPCVNGGTCQDGVNDYS
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99US-0123957P.
99US-0134287P.
99WO-US012252.
99US-0141037P.
99US-0144758P.
99WO-US020111.
99WO-US020594.
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The invention relates to novel human angiogenesis-associated proteins designated PRO proteins (AAB53064-B53097), and to nucleic acide encoding PRO proteins also relates to vectors and host cells comprising a PRO nucleic acid, the recombinant production of a PRO protein, agoniere or antagoniere of a PRO protein, agoniere or antagoniere of a PRO protein, adoniere acid, the recombinant production of a PRO protein, agoniere or antagoniere of a PRO protein, adoniere or antagoniere of a PRO protein, additionally encompasses methods of identifying modulators of PRO additionally encompasses methods of identifying modulators of PRO expression or activity; diagnosing a cardiovascular, endothelial or angiogenic disorder, or a susceptibility to such a disorder by detecting mutations in a PRO gene, or the expression level of a PRO gene within a particular tissue; treating a cardiovascular, endothelial or angiogenic disorder via the administration of a PRO protein, PRO nucleic acid; and methods of inhibiting or stimulating endothelial acid, and methods of inhibiting or stimulating endothelial acidies. PRO protein, or an agonist pRO proteins, PRO nucleic acids, PRO proteins, antibodies agints PRO proteins, endothelial or angiogenic disorders, such as atheracelerosis, osteoporosis, myocardial infarction, hypertension, alabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis, endometriosis, ulcers, wounds, cancer, Alzheimer's disease, psoriasis, endometriosis, ulcers, wounds, cancer, Alzheimer's disease, or stroke. PRO proteins, as hybridisation probes to screen libraries to isolate obnas with sequence identity to PRO proteins, and in gene therapy. PRO nucleic acids can also be used to produce transgenic animals useful for the development and secreening of potential independence rep
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                                               Gerber H, Goddard A;
Kuo SS, Mark MR, Marst
Williams PM, Wood WI;
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                                                                                                                                                                                                            New isolated nucleic acid for producing a PRO polypeptide, genetic disorders and treating cardiovascular, endothelial disorders, such as atherosclerosis, wounds or cancer.
                                                 Ferrara N,
Hillan KJ,
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                           Ashkenazi AJ, Baker
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Length 4, Score 3494.5; DB 4 Pred. No. 1.8e-190; 7; Mismatches 64; 84.1%; llarity 83.3%; Conservative 4 Query Match Best Local Similarity Matches 609; Conser Sequence 723 AA;

~ 120 113 180 173 240 233 300 360 293 9 GRTDLKY HGFCDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCT ENSYSCT GAGGGGC GRIDLKY Gaps 723; 11; MGGRFLLTLALLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGGGPG HGFCDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCN FTWPGTFSLIIEALHTDSPDDLTTENPERLISRLATORHLAVGEEWSQDLHSS HHKPCKNGATCTNTGQGSYTCSCRPGYTGSSCEIEINECDANPCKNGGSCTDL Indels 47; 301 174 н 61 **S** 121 114 181 241 234 g g 8 ઠ g Q ઠે S ઠે õ ઠે

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98WO-US019437.

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14-SEP-1998;
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99WO-US0010733.
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The invention describes an isolated nucleic acid (I) comprising, or which has 80 % sequence identity to, or the full-length coding sequence of, one of 275 nucleotide sequences, and which encodes a corresponding polypeptide selected from 275 amino acid sequences, where all sequences are given in the specification. The polypeptide encoded by (I) is used to detect PRO polypeptides, link a bioactive molecule to a cell expressing a PRO polypeptide, modulate a biological activity of a cell, stimulate the release of tumour necrosis factor (TNF)-alpha from human blood, modulate the proliferation or differentiation of cells or gene expression, stimulate the release of proteoglycans, stimulate the release of cytokine from peripheral blood mononuclear cells, inhibit the binding of A-peptide from peripheral blood mononuclear cells, inhibit the binding of A-peptide acid and polypeptide encoded by it, are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, acquired immunodeficiency syndrome (AIDS), cancer, or diabetic complications. The nucleic acid is useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. This is the amino acid sequence of a novel human secreted and
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Wood WI,
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17; Mismatches 64;
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IE, Goddard A, Godowski
tewart TA, Tumas D, Wat
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2001WO-US017800.
2001US-00874503.
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2001US-00887879.
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Human; PRO polypeptide; secreted and transmembrane protein;
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Wood WI,
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The present invention relates to the isolation of novel human PRO
polypeptides, and the polynucleotide sequences encoding them. The PRO
polypeptides are secreted and transmembrane proteins. The PRO
polypeptides are useful for detecting other PRO polypeptides, for linking
to polypeptides are useful for detecting other PRO polypeptides, for modulating
to bioactive molecules to cells expressing PRO polypeptides, for modulating
to biological activities of cells expressing PRO polypeptides, and for for
identifying agonists or antagonists. The PRO polypeptides are useful for
thuman blood, for stimulating the prosence of tumours. The polynucleotide
thuman blood, for stimulating the presence of tumours. The polynucleotide
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the preparation of PRO polypeptides, for generating transgenic
animals or knockout animals, for the genetic analysis of individuals with
genetic disorders, and in gene therapy. ABU66570-ABU66844 represent the
thuman PRO polypeptides of the invention. Note: The sequence data for this
patent was obtained in electronic format directly from the USPTO web site
at sequata.uspto.gov/psipsDIDEntry.html
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Sequence 2, Application US/09908322

Patent No. US20020107194A1

GENERAL INFORMATION:
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
Gray, Gras Byridon
Gray, Gras Byridon
Gray, Gras Byridon
VERTEBRAID BELTA GENE AND METHODS BASED THEREON
VUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
GTTAT: NY
COUNTRY: USA
ZIF: 100356/2711

COMPUTER RADABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: TBM Compacible
OPERATION VUMBER: US/09/908,322

CURRENT APPLICATION NUMBER: US/09/908,322

FILING DATE: 17-Jul-2001

CLASSIFICATION NUMBER: US/09/908,322

FILING DATE: Z-BEC-1997

ATTORNEY/AGENT INFORMATION:
RESTRANCE/POCKET NUMBER: 18,872

REFERENCE/POCKET NUMBER: 18,872

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REFERENCE/POCKET NUMBER: 1326-123
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TELEPHONE: 212-790-9090
TELEX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 728 amino acids
TYPE: amino acid
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Pred. No. 3e-266
Mismatches
                                                             Pinto
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                                                                                          Spyridon
                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/783,931
FILING DATE: 15-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-122
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-122
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                           Ish-Horowicz, David
Henrique, Domingos Manuel
Lewis, Julian Hart
Artavanis-Tsakonas, Spyric
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                                                                                                  Gray, Grace
INVENTION: ANTIBODIES TO
AND FRAGMENTS
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SOFTWARE: FastSEQ Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 728 amino acids
TYPE: amino acid
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Sequence 2, Application US/0978393
Publication No. US20030073620A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & E
STREET: 1155 Avenue o
CITY: New York
STATE: NY
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; SEQUENCE DESCRIPTION: SEQ
US-09-783-931-2
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Local Similarity 100.0%;
les 728; Conservative C
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RESULT 2 US-09-783-931

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                                                                                                 HHKPCKNGATCTNTGQGSYTCSCRPGYTGSSCEIEINECDANPCKNGGSCTDLENSYSCT
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of the America
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
RENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,32
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>
OR APPLICATION DATA:
APPLICATION DATA:
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'INVENTION: NUCLEOTIDE P
VERTEBRATE I
VERTEBRATE I
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Henrique, Domingos Ma
Lewis, Julian Hart
Artavanis-Tsakonas, S
Gray, Grace
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; Sequence 5, Application US/09908322
; Patent No. US20020107194A1
; GENERAL INFORMATION:
APPLICANT: ISh-Horowicz, Dav.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & E
STREET: 1155 Avenue o
CITY: New York
STATE: NY
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                               CPPGFYGKNCELSAMTCADGPCFNGGRCTDNPDGGYSCRCPLGYSGFNCEKKI
                                                                          CANGAQCVDLGNSYICQCQAGFTGRHCDDNVDDCASFPCVNGGTCQDGVNDYS
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Pred. No. 1.5e-265;
); Mismatches 0;
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Sequence 8, Application US/10417719
Fublication No. US20030180784A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc
APPLICANT: McCarthy, Sean
APPLICANT: Gearing, David
ITITLE OF INVENTION: HUMAN DELTA3 AND USES THI
FILE REFERENCE: MBIO1997-002CP2M
CURRENT APPLICATION NUMBER: US/10/417,719
CURRENT APPLICATION NUMBER: US/09/568,218
PRIOR FILING DATE: 2000-05-09
PRIOR FILING DATE: 1997-06-11
PRIOR FILING DATE: 1997-06-11
PRIOR FILING DATE: 1997-04-04
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 4.0
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.1 Similarity 99.9%;
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NUMBER
SOFTWARE: Fa.
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US-10-417
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COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                        STREET: 1155 Avenue o CITY: New York STATE: NY
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                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie
                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide;
SEQUENCE DESCRIPTION: EUS-09-783-931-5
                                                                                                              SEQUENCES:
                                                                                         Gray, Grainvention:
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                                                                                                TITLE OF
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                                                                                                                                             Length
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                                                                                                                                           ore 3495.5; DB ed. No. 9e-223; Mismatches 5
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Migrock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-123
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-869-8864
TELEFX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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02
                                                                                                                                             Score
Pred.
                                                                                                                      ID
                                                                                 LENGTH: 721 amino acids
TYPE: amino acid
                                                                                                 <Unknown>
                                                                                                                                                          65;
                                                                                                                      SEQ
                                                                                                                                            ch 84.2%; I Similarity 82.2%; 600; Conservative
                                                                                                 TOPOLOGY: vuknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: E
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                                                                                                STRANDEDNESS:
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                                                                               Ish-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.2%; Score 3495.5; Diarity 82.2%; Pred. No. 9e-223
Conservative 65; Mismatches
                                                                                                                                                                                                                                                                                                                             COMPUTER: DIBKELLE
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/783,931
FILING DATE: 15-Feb-2001
CLASSIFICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-122
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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RESULT 5
US-09-783-931-5
; Sequence 5, Application US/09783931
; Publication No. US20030073620A1
; GENERAL INFORMATION:
; APPLICANT: ISh-Horowicz, David Henrique, Domingos
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TYPE: amino acid
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Sequence 109, Application US/10042865

Publication No. US20040029216A1

GENERAL INFORMATION:

APPLICANT: Padigaru, Muralidhara
APPLICANT: Zerhusen, Bryan D
APPLICANT: Zerhusen, Bryan D
APPLICANT: Spytek, Kimberly
APPLICANT: Zhong, Mei
APPLICANT: Spytek, Kimberly
APPLICANT: Taylor, Sarah
APPLICANT: Patturajan, Meera
APPLICANT: Patturajan, Meera
APPLICANT: Taylor, Sarah
APPLICANT: Miller, Charles E
APPLICANT: Gerlach, Velizar T
APPLICANT: Gerlach, Valerie L
APPLICANT: Boldog, Karen
APPLICANT: Beleman, Karen
APPLICANT: Malyankar, Uriel M
APPLICANT: Malyankar, Uriel M
APPLICANT: Malyankar, Uriel M
APPLICANT: Malyankar, Uriel M
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Glennda
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T: Li, Li
T: Zerhusen, Bryan D
T: Casman, Stacie J
T: Shenoy, Suresh G
T: Shenoy, Suresh G
T: Shenoy, Suresh G
T: Shenoy, Rei
NT: Spytek, Kimberly
NT: Spytek, Kimberly
NT: Long, Mei
NT: Patturajan, Meera
NT: Poonet, Corine A.M
ANT: Tchernev, Velizar T
ANT: Tchernev, Velizar T
ANT: Miller, Charles E
CANT: Gerlach, Valerie L
CANT: Gerlach, Valerie L
CANT: Belierman, Raren
ICANT: Malyankar, Uriel M
ICANT: Malyankar, Uriel M
ICANT: Malyankar, Uriel M
ICANT: Malyankar, Uriel M
ICANT: Smithson, Glennda
ICANT: Smithson, Glennda
ICANT: Stone, David
LE OF INVENTION: Proteins, P
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Pred. No. 9e-223;
55; Mismatches 54
              865
FILE REFERENCE: 21402-537

CURRENT APPLICATION NUMBER: US/10/042,865

CURRENT FILING DATE: 2002-05-17

PRIOR APPLICATION NUMBER: 60/260,417

PRIOR APPLICATION NUMBER: 60/260,831

PRIOR APPLICATION NUMBER: 60/272,338

PRIOR FILING DATE: 2001-01-10

PRIOR APPLICATION NUMBER: 60/274,876

PRIOR APPLICATION NUMBER: 60/274,876

PRIOR FILING DATE: 2001-03-09

PRIOR FILING DATE: 2001-04-18

NUMBER OF SEQ ID NOS: 264

SOFTWARE: PACENTIN Ver: 2.1

SEQ ID NO 109

LENGTH: 721
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Query Match
Best Local Similarity 83.3%;
Matches 609; Conservative
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                                                                                                                                                        COMPOSITIONS
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О
                                                 Sequence 21, Application US/09828366;
Sequence 21, Application US/09828366;
Patent No. US20020010137A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Klein, Robert D.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Yuan, Jean
TITLE OF INVENTION: METHODS AND COMPOSITIONS
TITLE OF INVENTION: CELL GROWTH
FILE REFERENCE: P1694R1C1
CURRENT APPLICATION NUMBER: US/09/828,366
CURRENT FILING DATE: 2001-04-05
Prior filing data removed - refer to PALM or
NUMBER OF SEQ ID NOS: 29
LENGTH: 723
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EK-LEGQGGPFPWVAVCAGVILVLMLLLGCAAVVVCVRLRLQKHRPPADPCRGETETMNN
                                        LANCOREKDISISVIGATOIKNTNKKVDFHSDNS-DKNGYKVRYPSVDYNLVHELKNED
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Pred. No. 1e-222;
47; Mismatches 64;
                                                                                                                                                                                                                                   Sequence 9, Application US/09995593A

Sequence 9, Application US/09995593A

Patent No. US20020128197A1

GENERAL INFORMATION:

APPLICANT: SAKANO, SELJI

APPLICANT: TTOH, AKIRA

TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POI

FILE REFERENCE: KP8447DIV

CURRENT APPLICATION NUMBER: US/09/995,593A

CURRENT FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: 09/068,740

PRIOR FILING DATE: 1998-06-18

PRIOR FILING DATE: 1995-11-17

PRIOR FILING DATE: 1995-11-17

PRIOR FILING DATE: 1995-11-15

NUMBER OF SEQ ID NOS: 48

SOFTWARE: PATENTIN VET: 2.1

SEQ ID NO 9

LENGTH: 723
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R APPLICATION NUMBER: 60/062285

R APPLICATION NUMBER: 60/062285

R APPLICATION NUMBER: 60/062285

R FILING DATE: 1997-10-17

R APPLICATION NUMBER: 60/062814

R FILING DATE: 1997-10-24

R APPLICATION NUMBER: 60/063127

R APPLICATION NUMBER: 60/063129

R FILING DATE: 1997-10-29

R APPLICATION NUMBER: 60/063138

R FILING DATE: 1997-10-29

R APPLICATION NUMBER: 60/063138

R FILING DATE: 1997-10-29

R APPLICATION NUMBER: 60/063138

R FILING DATE: 1997-11-21

R APPLICATION NUMBER: 60/063138

R FILING DATE: 1997-11-22

R APPLICATION NUMBER: 60/063138

R FILING DATE: 1997-11-22

R APPLICATION NUMBER: 60/064248

R FILING DATE: 1997-11-22

R APPLICATION NUMBER: 60/065164

R FILING DATE: 1997-11-24

R APPLICATION NUMBER: 60/066314

R FILING DATE: 1997-12-11

R APPLICATION NUMBER: 60/06699

R FILING DATE: 1998-01-23

R APPLICATION NUMBER: 60/073019

R FILING DATE: 1998-02-09

R FILING DATE: 1998-02-09

R APPLICATION NUMBER: 60/073019

R APPLICATION NUMBE
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FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/079294
FILING DATE: 1998-03-25
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                             NGKNCSTPVSRCEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQG
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APPLICANT: Beres, Kevin P.
APPLICANT: Beres, Kevin P.
APPLICANT: Beres, Laura
APPLICANT: Penoyere, Laura
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Oiang
APPLICANT: Gadard, Madrey
APPLICANT: Gadard, Audiry
APPLICANT: Gadard, Madrey
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Sherwood, Steven
APPLICANT: Watanabe, Colin K
APPLICANT: WATANABER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 346, Application US/10028072 Publication No. US20030004311A1 GENERAL INFORMATION:
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EKDECVIATEV 723
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R APPLICATION NUMBER: 60/07
R FILING DATE: 1998-02-27
R FILING DATE: 1998-03-27
R APPLICATION NUMBER: 60/08
R FILING DATE: 1998-03-31
R APPLICATION NUMBER: 60/08
R FILING DATE: 1998-04-09
R APPLICATION NUMBER: 60/08
R FILING DATE: 1998-04-14
R APPLICATION NUMBER: 60/08
R FILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/08
R FILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/08
R FILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/08
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/08
R FILING DATE: 1998-05-15
R APPLICATION NUMBER: 60/08
R FILING DATE: 1998-06-10
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NUMBER: 60/0
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R APPLICATION NUMBER: 60/090863
R FILING DATE: 1998-06-26
R APPLICATION NUMBER: 60/091360
R FILING DATE: 1998-07-01
R APPLICATION NUMBER: 60/091519
R FILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091982
R PILING DATE: 1998-07-07 RESULT 10
US-10-140-808-346
; Sequence 346, Application US/10140808
; Publication No. US20030017563A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P. 47; Match 84.1% Local Similarity 83.3% Los 609; Conservative 72 ES. -≥ EKDECIIATE 61 55 174 234 593 59 653 718 -_ 21 114 241 94 361 81 474 534 601 81 301 54 421 414 541 713 4 9 Query Ma Best Loc Matches PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR 엄 ద 원 d d 셤 ద g 셤 ò ò ð 셤 ò ò ద ò 셤 ਨੇ ठे ठे ठ ò ठे ઠે

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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Godard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Aranabe, Colin K.
APPLICANT: Tumas, Daniel
APPLICANT: Abang, Zemin
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C182
CURRENT APPLICATION NUMBER: US/10/140,808
CURRENT FILING DATE: 2002-05-07
Prior Apploication removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
LENGTH: 723
                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                  Score 3494.5; DB 14;
Pred. No. 1e-222;
47; Mismatches 64;
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ilarity 83.3%;
Conservative 4
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609; Conserv
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Best Local S
Matches 609
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APPLICANT: Barer, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: DeForge, Laura
APPLICANT: Desonoyers, Luc
APPLICANT: Gao, Wei-Qiang
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timothy A.
APPLICANT: Watanabe, Colin K.
APPLIC
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                                MGGRFLLTLALLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGGGPGGAGQQQC
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Pred. No. 1e-222;
; Mismatches 64;
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Publication No. US20030022239A1
GENERAL INFORMATION:
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US-10-121-049-346
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VT: Beresini, Maureen

VT: Beresini, Maureen

VT: Beresini, Maureen

VT: Desnoyers, Luc

VT: Filvaroff, Ellen

Cao, Wei-Qiang

T: Gao, Wei-Qiang

T: Goddard, Audrey

T: Goddard, Audrey

V: Goddard, Austin L.

C: Sherwood, Steven

C: Sherwood, William

C: Shang, Zemin
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Sequence 346, Application US/
Publication No. US20030022331.
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timothy
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APPLICANT: Baker, Kevin P.
APPLICANT: Beroge, Laura
APPLICANT: Deforge, Laura
APPLICANT: Filvares, Luc
APPLICANT: Filvares, Luc
APPLICANT: Gao, Wei-Qiang
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timothy A.
APPLICANT: Wood, William
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Anny SECRETED AND TRANSMEMBRANE POI
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE REFERENCE: P33330R1C54
CURRENT APPLICATION NUMBER: US/10/123, 904
CURRENT APPLICATION NUMBER: US/10/123, 904
CURRENT APPLICATION NUMBER: US/10/123, 904
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Pred. No. 1e-222
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Publication No. US20030022328A1
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 550
EQ ID NO 346
LENGTH: 723
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C160 CURRENT APPLICATION NUMBER: US/10/140,470 CURRENT FILING DATE: 2002-05-06 Prior Application removed - See Palm or File Wr
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NUMBER OF SEQ ID NOS: 550
EQ ID NO 346
LENGTH: 723
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RESULT 14 US-10-175-746-346 ; Sequence 346, Application US/10175746

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  APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Geo, Wei-Qiang
APPLICANT: Goodwaki, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, William
APPLICANT: Shewart, Timochy A.
APPLICANT: Watanabe, Colin K
APPLIC
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Pred. No. 1e-222;
17; Mismatches 64;
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11 Similarity 83.3%;
609; Conservative
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US-10-175-746-346
L INFORMATION
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APPLICANT: Beresini, Maureen
APPLICANT: Beresini, Maureen
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gaowski, Paul J.
APPLICANT: Godwski, Paul J.
APPLICANT: Godwski, Paul J.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
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APPLICANT: Watanabe, Colin K

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Pred. No. 1e-222
47; Mismatches
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ilarity 83.3%;
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Publication No. US2003002'
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P
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283416 segs, 96216763 residues Searched:

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IS0719
C-Delta-1 - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09
C;Date: 150719
R;Henrique, D.; Adam, J.; Myat, A.; Chitnis, A.; Lewis, J.; Ish-Ho
Nature 375, 787-790, 1995
A;Title: Expression of a Delta homologue in prospective neurons in A;Reference number: IS0719; MUID:95319507; PMID:7596411
A;Reference number: IS0719; MUID:9656; EMBL:U26590; NID:9882411; PIDN
C;Superfamily: delta-4 protein; EGF homology <EGF1>
F;339-370/Domain: EGF homology <EGF2>
F;446-4485/Domain: EGF homology <EGF>
F;4454-485/Domain: EGF homology <EGF>
F;4454-485/Domain: EGF homology <EGF>
F;4454-485/Domain: EGF homology <EGF>
                                                                              _change
                                                                                                                                                    neurons
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Pred. No. 3.3e-242
0; Mismatches 0;
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0
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Best Local Similarity 100.0%;
Matches 728; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Delta-4 protein - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7570
R;Yoneya, T.; Tahara, T.; Nagao, K.; Yamada, Y.; Yamamoto, T.; Osawa, M.; Miyin S;Yoneya, T.; Tahara, T.; Taha
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                       72;
     THHKPCKNGATCTNTGQGSYTCSCRPGYTGSSCEIEINECDANPCKNGGS
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Pred. No. 1.1e-106;
.2; Mismatches 195;
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ilarity 48.2%;
Conservative 113
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Best Local Similarity
Matches 352; Conser
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JC7570
Delta-4 protein -
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148324
DELTA-like 1 - mouse
C; Species: Mus musculus (house mouse)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C; Accession: 148324
R; Bettenhausen, B.; de Angelis, M.H.; Simon, D.; Guenet, J.L.; Gossler, A.
Development 121, 2407-2418, 1995
A; Title: Translent and restricted expression during mouse embryogenesis of Dll1,
A; Reference number: 148324; MUID:95401858; PMID:7671806
A; Accession: 148324
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-722 < RES>
A; Cross-references: UNIPROT:Q61483; EMBL:X80903; NID:g806569; PIDN:CAA56865.1; E
C; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: Gelta-4 protein; EGF homology < EGF homo
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  CPPGFYGKNCELSAMTCADGPCFNGGRCTDNPDGGYSCRCPLGYSGFNCEKKID
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97;
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Pred. No. 2.2e-1971; Mismatches 6
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Best Local Similarity 79.5%;
Matches 581; Conservative
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QY 249 ECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCKNG 308	428 VDLGNSYICQCQAGFTGRHCDDNVDDCASFPCVNGGTCQDGVNDYSCTCPPGYNGKNCS- :: : :	544 TEGONSQFPWIAVCAGI-ILVLMLLLGCAAIVVCVRLKVQKRHHQPEACRSETETMNNLA : : :	661 KEEHGKCEAKCETYDSEAEEKSAVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISE 71	6 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	Qy 129 LIIEALHTDSPDDLTTENPERLISRLATQRHLAVGEEWSQDLHSSGRTDLKYSYRFVC 186

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SPNPCINGGSCQPSGKCICPAGFSGTRCETNIDDCLGHQCENGGTCIDMVNQYRCQCVPG
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                                             SLIIEALHTDSPDDLTTENPERLISRLATORHLAVGEEWSODLHSSGRTDLKYSYRFVCD
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R;Kopczynski, C.C.; Alton, A.K.; Fechtel, K.; Kooh, P.J.; Muskavitch, I Genes Dev. 2, 1723-1735, 1988
A;Title: Delta, a Drosophila neurogenic gene, is transcriptionally comp A;Reference number: A31246
A;Reference number: A31246
A;Molecule type: mRNA
A;Residues: 1-832 <KOP>
A;Coss-references: GB:Y00222
C;Genetics:
A;Gene: FlyBase:Dl
A;Cross-references: FlyBase:FBgn0000463
C;Superfamily: neurogenic protein delta; EGF homology
F;295-328/Domain: EGF homology <EGF1>
F;422-450/Domain: EGF homology <EGF>
F;533-564/Domain: EGF homology <EGF>
                                                                                                        FTGRHCDDNVDDCASFPCVNGGTCQDGVNDYSCTCPPGYNGKNCSTPVSRCEHN
           EHYYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDEQH
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Pred. No. 4.2e-86;
85; Mismatches 240;
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S00670
neurogenic repetitive locus delta protein precursor - fruit fly (Drosophila me neurogenic repetitive locus delta protein
N.Alternate names: gene Dl protein
C.Species: Drosophila melanogaster
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: S00670, A26637
R;Vaessin, H.; Bremer, K.A.; Knust, E.; Campos-Ortega, J.A.
EMBO J. 6, 3431-3440, 1987
A;Title: The neurogenic gene Delta of Drosophila melanogaster is expressed in A;Reference number: S00670
A;Accession: S00670
A;Accession: S00670
A;Accession: S0670
A;Molecule type: mRNA
A;Residues: 1-880 < VAE>
A;Cross-references uniPROT:P10041; EMBL:X06289; NID:G7852; PID:G7853
A;Cross-reference number: A91081; MUID:87218537; PMID:3107986
A;Accession: A26637
A;Molecule type: mRNA
A;Residues: A91081; MUID:87218537; PMID:3107986
A;Accession: A26637
A;Molecule type: mRNA
A;Residues: 422-436,'ET', 439-458,'A', 460-489,'T', 491-621 < KNU>
A;Cross-references: GB:X05140; NID:G7851; PIDN:CAA28786.1; PID:g929563
C;Genetics:
A;Gene: Delta; Dl
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A;Title: Jagged: a mammalian ligand that activates Notch1 A;Reference number: A56136; MUID:95211842; PMID:7697721 A;Accession: A56136
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A;Cross-references: FlyBase:FBgn0000463
C;Superfamily: neurogenic protein delta; EGF homology
C;Keywords: transmembrane protein
F;1-18/Domain: signal sequence #status predicted <SIG
F;19-88/Product: neurogenic repetitive locus delta pr
F;457-488/Domain: EGF homology <EGF1>
F;533-564/Domain: EGF homology <EGF2>
                                                                                                  Score 1555.5; DB
Pred. No. 4.4e-86,
85; Mismatches 24(
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995
C;Accession: A56136
R;Lindsell, C.E.; Shawber, C.J.; Boulter, J.; Weinn
Cell 80, 909-917, 1995
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A; Molecule type: mRNA
A; Residues: 1-1220 <LIN>
A; Cross-references: GB:L38483
F;379-410/Domain: EGF homology <F;492-523/Domain: EGF homology <F;634-665/Domain: EGF homology <
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C; Date: 31-Dec-1991 #sequence_revision 02-Aug-1994 #text_cha C; Date: 31-Dec-1991 #sequence_revision 02-Aug-1994 #text_cha C; Accession: S16148; A36666
R; Thomas, U.; Speicher, S.A.; Knust, E.
Development 111, 749-761, 1991
A; Title: The Drosophila gene Serrate encodes an EGF-like tra A; Reference number: S16148; MUID:91347903; PMID:1840519
A; Reference number: S16148; MUID:91347903; PMID:1840519
A; Residues: 1-1408 < THO1>
A; Residues: 1-1408 < THO1>
A; Residues: 1-1408 < THO1>
A; Reference number: S16878
A; Reference number: S16878
A; Reference number: S16878
A; Residues: 1-1351, T', 1353-1408 < THO2>
A; Residues: 1-1351, T', 1353-1408 < THO2>
A; Cross-references: EMBL:X56811; NID:98563; PID:98564
                            .72;
193;
    7
Match 32.1%; Score 1332.5; DB Local Similarity 41.9%; Pred. No. 1.5e-72; Les 236; Conservative 77; Mismatches 193
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                                                        PDGGYSCRCPLGYSGFNCEKKI DYCSSSPCANGAQCVDLGNSY I COCQAGFTGRHCDDNV
                                                                                                                                                  DDCASFPCVNGGTCQDGVNDYSCTCPPGYNGKNCSTPVSRCEHNPCHNGATCHERSNRYV
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             ECEAPHSAGIAANALLTTTATAIIGSNLSSTALLAALTSAVASTSLAIGPCINAKECRNQ
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A55845
C; Species: Xenopus laevis (African clawed frog)
C; Species: Xenopus laevis (African clawed frog)
C; Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_ch
C; Accession: A35844
R; Coffman, C.; Harris, W.; Kintner, C.
Science 249; 1438-1441, 1990
A; Title: Xotch, the Xenopus homolog of Drosophila notch.
A; Reference number: A15844; MUID: 90385285; PMID: 2402639
A; Accession: A35844
A; Status: preliminary; nucleic acid sequence not shown; not
A; Molecule type: mRNA
A; Residues: 1-2524 < COF>
C; Superfamily: Notch protein; ankyrin repeat homology; EGF
C; Keywords: transmembrane protein
F; 184-215/Domain: EGF homology < EGF1>
F; 184-215/Domain: EGF homology < EGF2>
F; 185-1956/Domain: EGF homology < EGF3>
F; 1951-1989/Domain: ankyrin repeat homology <AN1>
F; 1951-1989/Domain: ankyrin repeat homology <AN3>
F; 2024-2056/Domain: ankyrin repeat homology <AN3>
F; 2024-2056/Domain: ankyrin repeat homology <AN3>
F; 2024-2056/Domain: ankyrin repeat homology <AN4>
F; 2024-2056/Domain: ankyrin repeat homology <AN5>
F; 2057-2089/Domain: ankyrin repeat 
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-Oct-1990 #text_
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8; Mismatches 2
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Best Local Similarity 29.3%;
Matches 190; Conservative
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          R.J.; Scottgale, T.N.; Diederich, R.J.; Artavanis-Tsakona, 2188-2201, 1990
e. 2188-2201, 1990
e. gene Serrate encodes a putative EGF-like transmembrane
e. number: A36666; MUID:91099666; PMID:2125287
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,739,965,977,1004,1030,1150/Binding
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R;Fleming, R.J.; Scottgale, T.N.; Diederich, R.J.; Artavanis-Genes Dev. 4, 2188-2201, 1990
A;Title: The gene Serrate encodes a putative EGF-like transme A;Reference number: A36666; MUID:91099666; PMID:2125287
A;Accession: A36666; MUID:91099666; PMID:2125287
A;Actus: preliminary
A;Accession: A36666; MUID:91099666; PMID:2125287
A;Cross-references: GB:M35759; NID:g158605; PID:g158606
C;Genetics:
A;Gene: Flybase: Elybase: FBgn0004197
C;Keywords: glycoprotein; transmembrane protein
F;1-84/Domain: signal sequence #status predicted <SIG>F;1-84/Domain: signal sequence #status predicted <SIG>F;85-1408/Product: gene serrate protein #status predicted <F;85-1408/Domain: EGF homology <EGG1>F;85-148/Domain: EGF homology <EGG1>F;35-388/Domain: EGF homology <EGG0>F;35-388/Domain: EGF homology <EGG0>F;35-388/Domain: EGF homology <EGG0>F;35-488/Domain: EGF homology <EGG0>F;615-645/Domain: EGF homology <EGG1>F;615-645/Domain: EGF homology <EGG1>F;615-645/Domain: EGF homology <EGG1>F;81-94/Domain: EGF homology <EGG1>F;81-2-1060/Region: cysteine-rich
F;122-1246/Domain: transmembrane #status predicted <IMIT>F;122-11408/Domain: transmembrane #
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e H B	Oy 490 SRCEHNPCHNGATCHERSNRYVCECARGYGGLNCO 524 :
L; Accession: S42612 R; Bierkamp, C.; Campos-Ortega, J.A. Mech. Dev. 43, 87-100, 1993 A; Title: A zebrafish homologue of the Drosophila neurogenic gene Notch and its pattern c A; Reference number: S42612; MUID: 94128602; PMID: 8297791	RESULT 12 T31070 notch homolog - sea urchin (Lytechinus variegatus) C;Species: Lytechinus variegatus (variegated urchin) C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000 C;Accession: T31070
reliminary type: mRNA 1-2437 <bie> erences: UNIPROT: P46530 ly: notch protein; anky omain: EGF homology <eg< td=""><td>R;Sherwood, D.R.; McClay, D.R. Development 124, 3363-3374, 1997 Development 124, 3363-3374, 1997 A;Title: Identification and localization of a sea urchin Notch homologue: insights into A;Reference number: Z20966; MUID:97454256; PMID:9310331 A;Accession: T31070 A;Status: preliminary; translated from GB/EMBL/DDBJ</td></eg<></bie>	R;Sherwood, D.R.; McClay, D.R. Development 124, 3363-3374, 1997 Development 124, 3363-3374, 1997 A;Title: Identification and localization of a sea urchin Notch homologue: insights into A;Reference number: Z20966; MUID:97454256; PMID:9310331 A;Accession: T31070 A;Status: preliminary; translated from GB/EMBL/DDBJ
/Domain: EGF homology <egf2> /Domain: ankyrin repeat homology <an1 <an2="" <an3<="" ankyrin="" domain:="" homology="" repeat="" td=""><td>A;Molecule Lype: mkNA A;Residues: 1-2531 <she> A;Cross-references: EMBL:AF000634; NID:g2570350; PID:g2570351; PIDN:AAB82088.1 C;Superfamily: notch protein; ankyrin repeat homology; EGF homology</she></td></an1></egf2>	A;Molecule Lype: mkNA A;Residues: 1-2531 <she> A;Cross-references: EMBL:AF000634; NID:g2570350; PID:g2570351; PIDN:AAB82088.1 C;Superfamily: notch protein; ankyrin repeat homology; EGF homology</she>
/Domain: ankyrin repeat homology <an4> /Domain: ankyrin repeat homology <an5></an5></an4>	Query Match Best Local Similarity 30.6%; Pred. No. 7.3e-40; Matches 184; Conservative 80; Mismatches 231; Indels 106; Gaps 23;
Query March Best Local Similarity 27.3%; Pred. No. 1.1e-40; Matches 190; Conservative 69; Mismatches 195; Indels 241; Gaps	Qy 2 GGRFLLTLALLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRN 45 : : : : : : : : :
OY 12 LSALLCRCQVDGSG-VFELKLQEFVNKKGLLSNRNCCRGGGPGGAGQ 57 :::	Qy 46 CCRGGGPGGAGQQQCDCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFS 99
Qy 58 QQCDCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGA 107	100 VPDGAGGADPAFSNPIRFPFGFTWPGTFSLIIEALHTDSPDDLTTENPERLISR
Oy 108 DPAFSNPIRFPFGFTWPGTFSLIIEALHTDSPDDLTTENPERLISRLATQRHLAVGEEWS 167	154 LATQRHLAVGEEWSQDLHSSGR-TDLKYSYRFVCDEHYYGEGCSVFCRPR
Qy 168 QDLHSSGRTDLKYSYRFVCDEHYYGEGCSVFCRPRDDRFGHFTC 211 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	203DDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDEQHGFC
Qy 212 GERGEKVCNPGWKGQYCTEPICLPGC-DEQHGFCDKPGECKCRVGWQGRYC 261 Qy 12 GERGEKVCNPGWKGQYCTEPICLPGC-DEQHGFCDKPGECKCRVGWQGRYC 261 Db 11	245 DKPGECKCRVGWQGRYCDECIRYPGCLH-GTCQQPWQCNCQEGWGGLFCNQDL
Oy 262 DECIRYPGCLHGTCQOPWQCNCQEGWGGLFCNQDLNYCTHHKPCKNGATCT 312 :	OY 297 NYCTHHKPCKNGATCT-NTGQGSYTCSCRPGYTGSSCEIEINECDANPCKNGGSCTDLEN 355

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924-933/Disulf
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F;636-667/Domain: EGF homology <EG15>
F;712-743/Domain: EGF homology <EG15>
F;712-743/Domain: EGF homology <EG16>
F;750-781/Domain: EGF homology <EG17>
F;788-819/Domain: EGF homology <EG18>
F;886-857/Domain: EGF homology <EG19>
F;864-895/Domain: EGF homology <EG20>
F;864-895/Domain: EGF homology <EG21>
F;902-933/Domain: EGF homology <EG21>
F;902-933/Domain: EGF homology <EG21>
F;936-1064/Region: avidin-like
F;23-34,28-43,45-54,62-88,180-191,185-200,202-211,218-229,223-238,240-2
57,451-466,468-477,484-495/Disulfide bonds: #status predicted
F;28-504,506-515,522-533,527-542,544-553,560-571,565-580,582-591,598-6
08,810-819,826-837,831-846,848-857,864-875,869-884,886-895,902-913,907-
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Best Local Similarity 27.7%; Pred. No. 7.1e-40;
Matches 211; Conservative 78; Mismatches 294;
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Nichternate names: epidermal growth factor homolog precursor
Cispecies: Strongylocentrotus purpuratus (purple urchin)
Cipace: 11-May-192 Heaquence revision 17-Sep-1937 Heax—Change 09-Jul
Cipacesion: Addisis Hadia; Rollo, D.R.; Hutch, D.A.; Raff, R.A.
Aitle: Strongylocentrotus analysis of the uEGF gene in the sea urchin Strong
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Airtle: Dian, Andrews, M.E.; Raff, R.A.
Airtle: Avidin-like domain in an epiderral growth factor homolog regoles and analysis of homology regoles
Figs. 250 Homain: EGF homology regoles
Figs. 251 Homology regoles
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   QGSYTCSCRPGYTGSSCEIEINECDANPCKNGGSCTDLENSYSCTCPPGFYGKNCELSAM
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                                                                                                                                                                      SCRCPLGYSGFNCEKKIDYCS-SSPCANGAQCVDLGNSYICQCQAGFTGRHCDDNVDDCA
                                                                                                                                                                                                                                                          SFPCVNGGTCQDGVNDYSCTCPPGYNGKNCSTPVSRCEHNPCHNGATCHERSNRYVCECA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Experimental source: embryo
;Experimental source: embryo
;Note: sequence extracted from NCBI backbone (NCBIP:126158)
;Comment: This protein has many EGF repeats and lin-12/Notch repeats
;Comment: This protein is one of the neurogenic proteins controlling the
;Superfamily: Notch protein; ankyrin repeat homology; EGF homology
;143-174/Domain: EGF homology <EGF1>
;560-591/Domain: EGF homology <EGF>
;674-705/Domain: EGF homology <EGF3>
;712-743/Domain: EGF homology <EGK3>
;836-867/Domain: EGF homology <EGX3>
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                                                                                                                                                                                                                                                                                            Motch B protein - mouse (fragment)

Nylternate names: Notch homology

Cyspecies: Mus musculus (house mouse)

Cybate: 21-Jan-1994 #sequence revision 05-Jan-1996 #text_change

Cybatesion: A49175; PH1570; S32113

Rylardelli, W.; Lendahl, U.

Exp. Cell Res. 204, 364-372, 1993

A7Title: Motch A and Motch B--two mouse Notch homologues coexpre

A, Reference number: A49175; MUD: 93178563; PMID: 8440332

A, Accession: A49175

A, Residues: preliminary; nucleic acid sequence not shown

A, Molecule type: mana

A, Roserimental source: embryo

A, Experimental source: embryo

A, Note: sequence extracted from NCBI backbone (NCBIP: 12615)

A, Cromment: This protein has many EGF repeats and lin-1

C, Comment: This protein has many EGF repeats and lin-1

C, Supperfamily: Notch protein; ankyrin re-

C, Supperfamily: Notch protein; ankyrin re-

C, Supperfamily: BGF homology < EC**

F, 143-174/Domain: EGF homology

F, 142-13/Domain: EGF homology

F, 142-13/Domain: EGF homology

F, 142-141/This protein has many end the neurogeni-

F, 142-13/Domain: EGF homology

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F, 142-13/Domain: EGF homology
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(Species 10-589-199) Hacquence revision 10-589-1999 Htext_change 16-Mug-2 (Species 10-589-1999 Hackt_change 16-Mug-2 (Accession: Ad400; A24768; 503188; A05267

RAMAGO, A24768; 503188; A05267

RAMAGO, A24768; 503188; A05267

RAMAGO, S.; Kellby, M. R.; Young, M. W.

AACCESSION: AA4420; MUDD: 87064624; PMID: 3097517

AACCESSION: AA4420; MUDD: 87064624; PMID: 3097517

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ALIGNMENTS

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SEQUENCE FROM N.A.

TISSUE-Spinal cord;

MEDLINE-95319507; Pubmed=7596411;

MEDLINE-95319507; Pubmed=7596411;

Henrique D., Adam J., Myat A., Chitnis A., Lewis J., Ish-Horowicz D.;

"Expression of a Delta homologue in prospective neurons in the chick.";

"Auture 375:787-790(1995).

IL Nature 375:787-790(1995).

BMST, 150719; 150719; 150719.

R PIR; 150719; 150719; 150719.

R PIR; 150719; 150719; 150719.

R PIR; 150719; 150719; 150719.

R HSSP; MO0140; 1EDM.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0015620; C:membrane; IEA.

GO; GO:0015620; C:membrane; IEA.

GO; GO:0015620; F:calcium ion binding; IEA.

R HSSP; MO0175; F:calcium ion binding; IEA.

GO; GO:0007154; P:calcium ion binding; IEA.

R InterPro; IPR00184; EGF_2.

IN InterPro; IPR00184; EGF_1.

R InterPro; IPR00188; EGF_1.

R PROMO195; EGF; 1.

R PROSITE; PS001010; ASX HYDROXYL; 3.

R PROSITE; PS00101; ASX HYDROXYL; 3.

R PROSITE; PS01186; EGF_2; 6.

R PROSITE; PS01186; EGF_3; 6.

R PROSITE; PS01187; EGF_CA; 2.

R RCF-1ike domain.
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
NCBI_TaxID=9031;
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5; Mismatches 54;
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   Xenopus embryos
gene Delta.";
"Primary neurogenesis in Xenopus embryos the Drosophila neurogenic gene Delta."; Nature 375:761-766 (1995).

EMBL; L42229; AAC38017.1; -.

HSSP; P00740; 1EDM.

GO; GO:0016020; C:membrane; 1EA.

GO; GO:0005509; F:calcium ion binding; I GO; GO:0007154; P:cell communication; IE.

InterPro; IPR00152; Asx_hydroxyl_S.

InterPro; IPR00152; Asx_hydroxyl_S.

InterPro; IPR00174; DSL.

InterPro; IPR001438; EGF_Ca.

InterPro; IPR001438; EGF_Ca.

InterPro; IPR001438; EGF_II.

InterPro; IPR001638; EGF_II.

Pfam; PF01414; DSL; 1.

Pfam; PF01010; EGFBLOOD.

SMART; SM00051; DSL; 1.

PROSITE; PS00022; EGF_I; 8.

PROSITE; PS00186; EGF_Z; 8.

PROSITE; PS01186; EGF_Z; 8.

PROSITE; PS01186; EGF_Z; 8.

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X-Delta-1.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vert
Amphibia; Batrachia; Anura; Mesobatrachia; E
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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MEDLINE=95319507; PubMed=7596411;
Henrique D., Adam J., Myat A., Chitnis A.
"Expression of a Delta homologue in prosperick.";
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MEDLINE=95319503; PubMed=7596407
Chitnis A., Henrique D., Lewis J
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MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Chen J., Chow B., Chui C., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vangts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
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MEDLINE=99180765; PubMed=10079256;
Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,
Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas
"Human ligands of the Notch receptor.";
Am. J. Pathol. 154:785-794(1999).
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                                                                                                                                                                                                                                             Craniata, Vertebrata, Euteleostomi
Catarrhini, Hominidae, Homo.
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Han W., Ye Q., Moore M.A.S.;
"A soluble form of human delta-like-1 inhibits differentiation hematopoietic progenitor cells.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
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J. Exp. Med. 194:991-1001(2001).

-!- FUNCTION: Acts as a ligand for Notch receptors. Blocks the differentiation of progenitor cells into the B-cell lineage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The secreted protein discovery initiative (SPDI), a large-sca effort to identify novel human secreted and transmembrane proteininformatics assessment."; Genome Res. 13:2265-2270(2003).
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                                                                                                                                         DLL1 HUMAN STANDARD; PRT; 723 AA.
0005548; Q9NU41; Q9UJV2;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Delta-like protein 1 precursor (Drosophila Delta homolog (H-Delta-1) (UNQ146/PRO172).
                                                                                                                                                                                                                                                                                                                                                                                                                                              Oda T., Chandraseknarappa v.v., "Human Delta 1 gene sequence."; "Human Delta 1 gene sequence."; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
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MEDLINE=21464863; PubMed=11581320;
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Primates;
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Submitted (APR-2000)
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                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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promoting the memorance of a population of calls with the characteristics of a T-call precursor.

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LANCQREKDISVSIIGATQIKNTNKKADFHGDHSADKNGFKARYPAVDYNLVQDLKGDDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Japanese common newt).
Chordata; Craniata; Vertebrata; Euteleostomi;
Caudata; Salamandroidea; Salamandridae; Cyno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      726;
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databases.
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Last sequence update)
Last annotation update
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Nakamura K., Kikuchi Y., Susaki K., Chiba C., Sai Submitted (OCT-2002) to the EMBL/GenBank/DDBJ dat -! - SIMILARITY: Contains 8 EGF-like domains.
EMBL; AB095017; BAC41350.2; -.
HSSP; P00740; IEDM.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0007154; P:cell communication; IEA.
InterPro; IPR00152; Asx hydroxyl_S.
InterPro; IPR001774; BGF_2.
InterPro; IPR001774; BGF_2.
InterPro; IPR001438; EGF_1I.
InterPro; IPR006209; EGF_1I.
InterPro; IPR006209; EGF_1I.
InterPro; IPR006209; EGF_1I.
InterPro; IPR006209; EGF_1I.
SMART; SM0019; EGF_6.
Pfam; PF001414; DSL; 1.
Pfam; PF001019; EGF_6.
PROSITE; PS00010; ASX HYDROXYL; 3.
PROSITE; PS0010; ASX HYDROXYL; 3.
PROSITE; PS0010; ASX HYDROXYL; 3.
PROSITE; PS01186; EGF_2; 7.
PROSITE; PS01187; EGF_CA; 2.
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nes 603; Conservative 4
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Eukaryota; Metazoa; Ch
Amphibia; Batrachia; C
NCBI_TaxID=8330;
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EKDECVIATEV
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Ligand Delta-1.
Name=Delta-1;
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Pred. No. 1.1e-218;
; Mismatches 66;
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  analysis
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                                     SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Mouse;
Strausberg R.;
Submitted (SEP-2003) to the EM
[3]
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Mouse;
Strausberg R.;
Submitted (JAN-2004) to the EM
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nes 581; Conservative
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  "Generation and initial
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SEQUENCE FROM N.A.

STRAIN=C57BL/6; TISSUE=Mouse;

X Rausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Boatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; N
VČBI_TaxID=10090;
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Pred. No. 1.1e-218;
72; Mismatches 66;
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SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Mouse;
Strausberg R.;
Strausberg R.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ
EMBL; BC057400; AAH57400.1; -.
SEQUENCE 722 AA; 78449 MW; 9D570B9DC7EEC7
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STRAIN=C57BL/6; TISSUE=Mouse;

X MEDLINE=22388257; PubMed=12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.

A Jones S.J., Maxra M.A.;

Jones S.J., Maxra M.A.;

"Generation and initial analysis of more than 15,000 full-length hume
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    THHKPCKNGATCTNTGQGSYTCSCRPGYTGSSCEIEINECDANPCKNGGSCTDE)
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:. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                               Euteleosto; Murinae;
                                                                               SEQUENCE FROM N.A.
STRAIN=C57BL/6J;
Nagaraja R., Waeltz P., Brathwaite M.E.;
Nagaraja R., Waeltz P., Brathwaite M.E.;
"Genomic Sequence Analysis in the Mouse t-complex Region.";
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
[2]
SEQUENCE FROM N.A.
STRAIN=C57BL/6J;
Brathwaite M., Waeltz P., Dudekula D., Nagaraja R.;
STRAIN=C57BL/6J;
Brathwaite M., Waeltz P., Dudekula D., Nagaraja R.;
SUBmitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY497019; AAR30869.1; -.
SEQUENCE 722 AA; 78449 MW; 9D570B9DC7EEC75E CRC64;
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                             Craniata; Vertebrata; E
Sciurognathi; Muridae;
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Pred. No. 1.1e-218;
72; Mismatches 66;
                                                                                                                                                                                                                                                                                                      72;
      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata
Mammalia; Eutheria; Rodentia
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                           Match 82.1%;
Local Similarity 79.5%;
nes 581; Conservative 7
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SEQUENCE FROM N.A.

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STRAIN=C57BL/6; TISSUE=Mouse;

X STRAIN=C57BL/6; TISSUE=Mouse;

X STRAIN=C57BL/6; TISSUE=Mouse;

X STRAIN=C57BL/6; TISSUE=Mouse;

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.J., Namer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human mand initial analysis of more than 15,000 full-length human
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Id. Sci. U.S.A. 99:16899-16903(2002)
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Pred. No. 1.1e-218;
; Mismatches 66;
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Submitted (JAN-2004) to the EMBL/GenBank/DDBJ
EMBL; BC065063; AAH65063.1; -.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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STRAIN=C57BL/6; TISSUE=Mouse;
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X STRAIN-E-57BL/6 X BALB/c; TISSUE=Embryo;

X MEDLINE=95401858; PubMed=7671806;

Bettenhausen B., de Angelis M.H., Simon D., Guenet J.-L., Gossler A.;

Bettenhausen B., de Angelis M.H., Simon D., Guenet J.-L., Gossler A.;

Transient and restricted expression during mouse embryogenesis of

Dll1, a murine gene closely related to Drosophila Delta.";

Development 121:2407-2418(1995).

-!- FUNCTION: May be involved in cell-to-cell communication in mammalian embryos. May have a role in cellular interactions

C -!- FUNCTION: May be involved in cellular interactions

C -!- SUBCULIVIAR LOCATION: Type I membrane protein.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- TISSUE SPECIFICITY: In the embryo, expressed in the paraxial mesoderm and nervous system. Expressed at high levels in adult heart and at lower levels, in adult lung.

-!- DEVELOPMENTAL STAGE: Expressed until day 15 in the embryo.

Expression then decreases and increases again in the adult.

-!- SIMILARITY: Contains 8 EGF-like domains.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                                                        use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.clor send an email to license@isb-sib.ch).
                   TCPPGFYGKNCELSAMTCADGPCFNGGRCTDNPDGGYSCRCPLGYSGFNCEKKI
                                                           PCANGAQCVDLGNSYICQCQAGFTGRHCDDNVDDCASFPCVNGGTCQDGVNDYS
                                                                      YNGKNCSTPVSRCEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQG
                                                                                                              TEKYTEGONSOFPWIAVCAGIILVLMLLLGCAAIVVCVRLKVOKRHHOPEACRS
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THHKPCRNGATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDI
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01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Delta-like protein 1 precursor (Drosophila Delta homolog 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no resti
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Sciurognathi; Murida
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            DB 1;
..7e-218;
les 67;
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            Score 3407; D
Pred. No. 1.7e
1; Mismatches
                    71;
476 N
78448 MW;
            Query Match
Best Local Similarity 79.5%;
Matches 581; Conservative
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722 AA;
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B. Dishio G., Whenli L., Boulter J., Weinmaster G.;

B. Dishio G., Whenli L., Boulter J., Weinmaster G.;

Submitted (DEC-1996) to the ENGL/GenBank/Dogs datebases.

C. -- FUNCTION: May be involved in cell-Liber.cell communication in many and a role in cellular interactions of a cellular interaction of a cellular interactions of a cellular interaction of cellular interaction interact
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Q8UWJ4;
Q8UWJ4;
Q8UWJ4;
Q8UWJ4;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DeltaD protein.
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID=7955;
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Pred. No. 1.1e-195;
1; Mismatches 95;
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Bevelopment 129:4773-4784 (2002).

EMBL; AF426384; AAL31528.1; -.

HSSP; P00740; 1EDM.

GO; GO:0016020; C:membrane; 1EA.

GO; GO:0005509; F:calcium ion binding; 1E

GO; GO:0007154; P:cell communication; 1EA

InterPro; 1PR00152; A8x_hydroxyl_S.

InterPro; 1PR00174; DSL.

InterPro; 1PR00143; EGF_Ca.

InterPro; 1PR001438; EGF_II.

InterPro; 1PR001438; EGF_II.

InterPro; 1PR006209; EGF_II.

Pfam; PF01414; DSL; 1.

Pfam; PF010008; EGF_EI.

Pfam; PF01010; EGFBLOOD.

SMART; SM00179; EGF_CA; 4.

PROSITE; PS00119; EGF_Z; 8.

PROSITE; PS001186; EGF_Z; 8.

PROSITE; PS01187; EGF_CA; 2.

EGF-like domain.

SEQUENCE 720 AA; 79380 MW; DE6B7393E2
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MEDLINE=22248969; PubMed=12361969,
Hans S., Campos-Ortega J.A.;
"On the organisation of the regula
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Pred. No. 1.7e-195,
81; Mismatches 95
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PROSITE;
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EGF-like
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PRELIMINARY; PRT; 717 AA.
P87357;
O1-MAY-1997 (TrEMBLrel. 03, Last sequence update)
T 01-MAY-1997 (TrEMBLrel. 26, Last sequence update)
T 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
T 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
E DeltaD transmembrane protein precursor.
Name=dld; Synonyms=deltaD;
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
K NCBI_TaxID=7955;
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SEQUENCE FROM N.A.

MEDLINE=97346722; PubMed=9203139;

MEDLINE=97346722; PubMed=9203139;

Dornselfer P., Takke C., Campos-Ortega J.A.;

Dornselfer P., Takke C., Campos-Ortega J.A.;

"Overexpression of a zebrafish homologue of the Drosophila neurons and som development.";

Mech. Dev. 63:159-171(1997).

Mech. Dev. 63:160-171(1997).

Mech. Dev. 63
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                                                                                         TISSUE=Embryo;

MEDLINE=22388257; Pubmed=12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.I.

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.

Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length hum

"Generation and initial analysis of more than 15,000 full-length hum
                                                                                                                                 .D.,
               (Danio rerio).; Craniata; Vertebrata; Euteleostomi; Teleostei; Ostariophysi; Cypriniform
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Strausberg R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
EMBL; BC075742; AAH75742.1; -.
Hypothetical protein.
SEQUENCE 772 AA; 84968 MW; 716A014158938576 CRC64;
                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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116;
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Best Local Similarity 65.5%; Pred. No. 6e-186; Matches 516; Conservative 77; Mismatches 11
Hypothetical protein.
Brachydanio rerio (Zebrafish) (Eukaryota; Metazoa; Chordata; Cactinopterygii; Neopterygii; Te
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TISSUE=Embryo;
MEDLINE=22341132; PubMed=12454917
Klein S.L., Strausberg R.L., Wagne
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PRINTS; PR00010; EGFBLOOD.
SMART; SM00051; DSL; 1.
SMART; SM00179; EGF CA; 3.
PROSITE; PS00010; ASX HYDROXYL; 2
PROSITE; PS01186; EGF 1; 8.
PROSITE; PS01186; EGF 2; 7.
PROSITE; PS01187; EGF 2; 7.
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Dev. Dyn. 225:384-391(2002)
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                                 GRFLLTLALLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGGGPGGA
                                           NGAQCVDLGNSYICQCQAGFTGRHCDDNVDDCASFPCVNGGTCQDGVNDYSCT
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Q1-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
MGC52561 protein.
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Xenopous Netazoa; Chordata; Craniata; Vertebrata; Eute Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pir Xenopodinae; Xenopus.
NCBI_TaxID=8355;
 DB 2;
le-181;
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Score 2854.5;
Pred. No. 1.1e
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               78;
Query Match
Best Local Similarity 66.4%;
Matches 502; Conservative
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MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Schemutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Klein S., Strausberg R.;

Submitted (JAN-2003) to the EMBL/GenBank/
EMBL; BC044262; AAH44262.1; -.

HSSP; P00740; 1EDM.

GO; GO:0016020; C:membrane; 1EA.

GO; GO:0005509; F:calcium ion binding; 1EP

InterPro; IPR00152; Asx_hydroxyl_S.

InterPro; IPR00174; DSL.

InterPro; IPR00142; EGF_2.

InterPro; IPR001438; EGF_II.

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M-Delta-1 Mouse not

M-delta-1 polypeptide (AAW11720) is the mouse homologue of Drosophila Delta, a protein that binds to Notch protein. It is expressed primarily in presomitic mesoderm, the central and peripheral nervous systems, and kidney. Chick (AAW11719) and human (AAW11721- 38) Delta-1 polypeptides have also been identified. Delta-1 proteins can be used to treat or prevent disorders characterised by increased Notch activity, such as cervical, breast, lung or colon cancer, melanoma or seminoma, as well as nervous system disorders, and to promote tissue regeneration and repair

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ligand; Parkinson's disease; Huntington's disease; motor neuron
heart disease; diabetes; liver disease; cirrhosis; renal disease
acquired immunodeficiency syndrome.
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The invention relates to modulating the differentiation of an embryonic stem cell; comprising: (a) providing a culture of embryonic stem cells; (b) providing at lease one ligand or its active binding fragment, capable of binding its cognate receptor polypeptide expressed by the embryonic cream cells, comprising an culture comprising embryonic stem cells and the ligand; and (d) growing a culture comprising embryonic stem cells, comprising (a) providing a culture comprising caid endealed are: (i) indiang the differentiation of embryonic stem cells, comprising; (a) providing a cell transfected with a mucleic acid sequences; (ii) an uncleic acid molecule which are applied of modulating embryonic stem cell; and which encodes a ligand capable of modulating embryonic stem cell; and (d) with an embryonic stem cell; and (d) growing the culture for the maintenance and/or differentiation of the embryonic stem cell; and (d) growing the culture for the maintenance and/or differentiation of the embryonic stem cell; in an undifferentiate are inhibitors of the maintenance of embryonic stem cells; and (c) growing the culture for the maintenance and propagated or its active comprising the cells; and (c) growing the cell; and (c) growing the cells; and (c) growing the cells; or comprising the cells; and (d) with an and differentiated erace; or (i) Inhibiting peth differentiation of embryonic stem cells; or comprising the cells; and (e) growing a culture for the maintenance of embryonic stem cells in an undifferentiated erace; or (i) Inhibiting with the signalling; and inhibitors of the methods cited above. The therapeutic cell of the comprising the cell identified in (a) with an embryonic stem cells or comprising the cell identified in (a) with an embryonic stem cells or cell and or or the sequences of (i) or (ii) the therapeutic cell or cell or cell or cell or cell or methods cited above. The therapeutic cell or cell or cell which have been induced to differentiate into an induced to differentiate in the present invention is use
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23-MAR-2001; 2001GB-00007299
17-APR-2001; 2001GB-00009346
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The present invention relates to a novel screening method which enables the identification of biologically active agents which mediate their effect through the activation of genes. The method involves providing a population of cells stably transfected with a nucleic acid encoding a reporter molecule, cloning the transfected with a nucleic acid encoding a reporter molecule, cloning the transfected with a nucleic acid encoding a caporter molecule as a result of exposure to the signal generated by the reporter molecule as a result of exposure to the agent. The method is useful in identifying biologically active agents and the genes through which the agents act, in screening potential drugs for their ability to activate certain drug targets in a high-throughput assay, in identifying relationships between signalling pathways and specific signals that could be useful in eventually directing the differentiation of embryonic stem cells and in toxicology assays by testing for unwanted activation or inhibition of specific signalling pathways. The present sequence is murine notch ligand delta-like I protein used to illustrate the method of the invention
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                                                                                                                                       Identifying biologically active agents comprises cloning transfected cells into a cell array, exposing the array to an agent to be tested, detecting signals generated by a reporter molecule as a result of exposure to the agent.
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Pred. No. 3.7e-225;
1; Mismatches 16;
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Matches 702; Conservative
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VSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDLSERI
                   GPFPWVAVCAGVVLVLLLLGCAAVVVCVRLKLQKHQPPPEPCGGETETMNNLA.
                                                                                                                                          Murine delta protein amino acid sequence.
                                                                                                             AAY79028 standard; protein; 722 AA
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Delta; Kuz; Notch; differentiation; cervical; breast; colon; cancer; lung; melanoma; seminoma; central nervous system disorder; psoriasis; tissue regeneration; liver cirrhosis; keloid formation; baldness; inner ear disorder; mouse.

WO200002897-A2 Mus sp

20-JAN-2000

99WO-US015817 13-JUL-1999 98US-0092513P 98US-0104834P 3-JUL-1998; 9-OCT-1998;

(UYYA) UNIV

Ξ ö Ψ Ω Rand Artavanis-Tsakonas S,

WPI; 2000-282852/24

liagnosis, 18 system, ซ central nervou New cleavage peptide, nucleic acids and antibodies useful for prevention and treatment of cancer, disorders of central nervo cirrhosis and psoriasis

3; 177pp; English. Claim 1; Fig This sequence represents the murine delta protein amino acid sequence.

C Delta is a toporythmic protein that contains a sequence which is cleaved

C by the metalloprotease-disintigrin Kuzbanian (Kuz). Cleavage by Kuz

C results in two fragments, a soluble amino terminal fragment consisting

C sesentially of the extracellular domain, and a membrane bound fragment

C consisting of the transmembrane domain and the intracellular domain. The

soluble fragment is able to bind to Notch. Delta plays a key role in

differentiation, and therefore detection and measurement of delta

activation is important in the study of differentiation. The invention

C relates to the delta cleavage peptides (the active fragment), and to

methods for detecting and measuring delta activation. Delta cleavage

C methods for detecting are useful for modulating the activity of

Notch, delta or kuz or at least one of the signalling pathways in a cell

Or or organism, expressing Notch. By contacting a cell with kuz protein or activity of in a cell

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RDTKCQSQSLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVIAT

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nucleic acid or its antibody, the activity or levels of delta protein is modulated and vice versa. A delta cleavage peptide or its derivative capable of binding kuz protein is useful for treating or preventing a disease or disorder associated with increased delta activity or expression such as cervical, breast, colon or lung cancer, melanoma or seminoma in humans. A recombinant cell comprising a delta peptide is useful for treating or preventing central nervous system disorders. A delta cleavage peptide is useful for the diagnosis of diseases or disorders associated with increased levels of Notch-delta protein binding activity comprising measuring the ability of delta cleavage peptides in a sample to bind kuz protein. A complex of delta protein and kuz is useful for diagnosing or screening for the presence of, or predisposition to developing a disease or disorder associated with aberrant levels of the complex, comprising measuring the level or functional activity of the complex, comprising measuring the level or functional activity of the complex or RNA encoding delta or kuz in a sample. The delta cleavage peptide is also useful for promoting tissue regeneration and repair, for treating liver cirrhosis, keloid formation, psoriasis, baldness and degenerative or traumatic disorders of the sensory epithelium of the
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5; Mismatches 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a polypeptide which suppresses proliferation and differentiation of undifferentiated cells such as neurons and blood cells. The polypeptide may be used for the prevent and control of disorders involving undifferentiated cells, such as leukaemia and malignant tumours, and improvement of blood formation, after immunosuppression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 Peptide(s) encoded by human genes delta-1 and serrate-1 - suppress proliferation and differentiation of undifferentiated human blood
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87.0%; Pred. No. 3.8e-205;
ive 46; Mismatches 45;
                                                                                                                                               Proliferation; differentiation; suppression;
blood cell; neuron; leukaemia; malignant tum
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                                    This sequence represents the human delta-1 protein, which is a ligand of the human notch protein. The protein or fragments, especially AAW75493-W75495, can be used as a drug to control vascular cells. The sequences were isolated and the truncated fragments were generated using the primers AAX16818-X16831
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             which
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                                                                                    Length
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             polypeptide
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Pred. No. 3.8e-205;
; Mismatches 45;
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             compri
             as drug
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            ar cell controlling ligand and is used
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The present invention describes full length and shortened human delta-2 proteins. Human delta-2 is a differentiation inhibitor which inhibits the differentiation of undifferentiated cells (other than brain or muscle cells), such as blood cells, and enhances the proliferation of undifferentiated blood cells. Products of human delta-2 may be used for the treatment of diseases such as leukaemia and malignant tumours. They may also be used in the culture of human cells in vitro, e.g. for production of supplies of undifferentiated blood cells. The present sequence represents human delta-1, from an example of the present
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Pred. No. 3.8e-205;
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leukaemia; malignant tumour
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241 GECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCKN 300	1 H H	Domain) = C
300 GATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSCTCPPGFYG 359	T.F.	Modified-site	/label= EGF- 252261
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360 KVCELSAMICADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCGSSPCSNGAKC 419 	FT ET	Domain	286 286
AICELSAMICADGPCFNGGRCSDSPDGGISCRCPVGISGFNCBRAIDICSSSPCSNGARC	T. H.	Modified-site	ຼຸຕ
20 VDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSA	T E	Modified-site	ູ ຕ
21 VDLGDAYLCRCQAGFSGRHCDDNVDDCASSPCANGGTCRDGVNDFSCTCPPGYTGRNCSA	FT	Modified-site	ູຸຕ
PVSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDLSERHMESQ	FT		/note= "N-my 310316
PVSRCEHAPCHNGATCHERGHRYVCECARGYGGPNCQFLLPELPPGPAVVDLTEK-LEGQ	F F F F F	Domain	/note= "N-my 314326
540 GGPFPWVAVCAGVVLVLLLLGCAAVVVCVRLKLQKHQPPFEPCGGETETMNNLANCQRE 599	14 14 14 14 14 14 14 14 14 14 14 14 14 1	Modified-site	/label= EGF- 328334
GGEFFWWAVCAGVILVLITTLEGCAAVVVCVRLKLQRARFALFCRGBIBIMNLANCQRE	- F-	Modified-site	340346
600 KDVSVSIIGATQIKNTNKKADFHGDHGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHS 659 	7 H H	Modified-site	/note= "N-my 342346 /note= "Case
KRDTKCOSO-SLOEKRRSPOHLGVGRF1, TENRPESVYSTSKDTKYOSVYVI, SAEKDECVI	FF	Modified-site	343355 /note= "Agn
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tion; cancer; neoplasia; tumour; breast; ovary;	- E- E-	Modified-site	/nore= "case 458480 /label= Agn
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Wermatological; antiarthritic; antirheumatic; immunosuppressive;

haemostatic; antiithyroid; antidiabetic; nootropic; neuroprotective;

matianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;

wattiansthmatic; systemic lupus erythematosus; rheumatoid arthritis;

Westeoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;

Westemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;

Westemic vasculitis; autoimmune-mediated skin disease;

Winflammatory bowel disease; dluten-sensitive enteropathy;

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RVCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGGGADSAFSNPIRFPFGFTWPGTF

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The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's systemic solerosis, idiopathic inflammatory myopathies, Sjogren's systemic succlimmune thrombocytopaenia, thyroiditis, diabetes mellitus, anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune cor immune-mediated skin diseases, allergic diseases, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease. AACS8397 to AACS8378 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AACS8579 to AACS8642 and AAB33414 to AACS8577 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sixty four PRO polypeptides, useful in the diagnosis and treatuimmune related disorders, e.g. systemic lupus erythematosis, rlarthritis, osteoarthritis, thyroiditis and diabetes mellitus.
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| WI, Yan M;
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larity 87.0%; Pred. No. 3.8e-205;
Conservative 46; Mismatches 45;
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Wood WI,
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an J, Pennica |
Watanabe CK, 1
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99WO-US020594.
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99WO-US021090.
99WO-US021547.
99WO-US023089.
99WO-US028113.
99WO-US028313.
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99WO-US028313.
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Kabakoff RC,
01-SEP-1999;

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30-NOV-1999;

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PRO211; PRO228; PRO538; PRO172; PRO182; neoplasia; inhibition; tumour; treatment; therapy; agonist; antibody; breast cancer; ovarian cancer; renal cancer; colorectal cancer; uterine cancer; prostate cancer; lung cancer; bladder cancer; melanoma; leukaemia; inflammatory disorder angiogenic disorder; immunologic disorder; human.
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 99WO-US005028.
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99US-0131445P.
99US-0134287P.
99US-0141037P.
99US-0144758P.
99WO-US020111.
99WO-US020594.
99WO-US020594.
99WO-US021090.
99WO-US021090.
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Local Similarity 87.0%;
nes 630; Conservative '
                                                                                                                                                                                                                                                       Nucleic acids encoding PRC and treating diagnosing a disorders in mammals.
                                                                                                                                                                                  Ashkenazi AJ, Baker KP,
Goddard A, Godowski PJ,
Smith V, Watanabe CK,
                                                                                                                                                                GENENTECH INC
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N-PSDB; AAA77512.
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23-JUN-1999;
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26-JUL-1999;
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08-SEP-1999;
13-SEP-1999;
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note= "N-glycosylation site"
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Isolated PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptides or their agonists (preferably anti-PRO agonist antibody or a small molecule mimicking the biological activity of PRO polypeptide) are useful in vitro or in vivo for inhibiting the growth of a tumour cell. Compositions comprising the PRO polypeptides are useful for inhibiting neoplastic cell growth and for treating cancer including breast, ovarian, renal, colorectal, uterine, prostate, lung, bladder, central nervous system cancer, melanoma and leukaemia in a mammal. The PRO polypeptides are also useful for treating other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal, blastocoelic disorders and inflammatory, angiogenic and immunologic disorders as well as being useful for identifying agonists to PRO polypeptides by contacting the polypeptide with a candidate molecule and monitoring biological activity mediated by the polypeptide
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AAU12172-AAU12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-consistential cells, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor vila. The PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy
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15-MAR-2000;

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17-MAY-2000;

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              RVCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPGTF
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MGSRCALALAVLSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGGAGPPP
                                                                                                           GECKCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCT
                                                                                                                                           GATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSCT
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The invention relates to novel human angiogenesis-associated proteins designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding PRO proteins. The invention also relates to vectors and host cells comprising a PRO nucleic acid, the recombinant production of a PRO protein, PRO antibodies specific for a PRO protein, fusion proteins comprising a PRO nucleic acid, and antagonists of a PRO protein, and comprising a PRO protein, and additionally encompasses methods of identifying modulators of PRO additionally encompasses methods of identifying modulators of PRO additionally encompasses methods of identifying modulators of PRO expression or a susceptibility to such a disorder by detecting mutations in a PRO gene, the administration of a PRO protein, and otherlial or angiogenic disorder via the administration of a PRO protein, PRO nucleic acid, and methods of inhibiting or stimulating endothalial and protein and PRO administration of a PRO protein, and proteins, PRO nucleic acids, PRO proteins, and proteins and PRO proteins, and proteins, and proteins, and proteins and PRO proteins, and proteins, and administration of a PRO proteins, and administration of strokens, mycardial infarction, bypertension, diabetic retinopathy, rheumatoid arthritis, Crohn's disease, bost stroke. PRO nucleic acids are additionally useful in the recombinant production of PRO proteins, a shybridisation probes to erreen libraries to isolate cDNA with sequence identity to PRO proteins, to analyse genetic disease, or stroke. PRO nucleic acids are additionally to PRO proteins, to enalyse genetic disease, or stroke. PRO proteins, to analyse genetic disease, and in gene therapeutic agents to an also be used to produce transgenic agents. The present sequence represents an enceding and additional and secure a
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.rk MR, Marsters
.wood WI;
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Kuo SS, Mark
Williams PM, Wo
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AL, Hillan KJ,
Watanabe CK,
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                                                                 99WO-USO05028.
99US-0123957P.
99US-0134287P.
99WO-US012252.
99US-0141037P.
99WS-0144758P.
99WO-US020111.
99WO-US020594.
99WO-US021547.
99WO-US023089.
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PJ, Gurney
, Pitti RM,
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N-PSDB; AAC97368.
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12-MAR-1999;
02-JUN-1999;
23-JUN-1999;
26-JUL-1999;
26-JUL-1999;
01-SEP-1999;
08-SEP-1999;
15-SEP-1999;
15-SEP-1999;
30-NOV-1999;
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98WO-US0119137.
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99WO-US022841.
99WO-US0228551.
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99WO-US0228634.
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99WO-US02864.
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99WO-US02864.
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The invention describes an isolated nucleic acid (1) comprising, or which has 80 % sequence identity to, or the full-length coding sequence of, one of 275 nucleotide sequences, and which encodes a corresponding cof 275 nucleotide selected from 275 amino acid sequences, where all sequences are given in the specification. The polypeptide encoded by (1) is used to detect PRO polypeptides, link a bioactive molecule to a cell expressing a PRO polypeptide, modulate a biological activity of a cell, stimulate the release of tumour necrosis factor (TNF)-alpha from human blood, modulate the uptake of glucose or free fatty acid by cells, stimulate or inhibit the uptake of glucose or free fatty acid by cells or gene expression, stimulate the release of proteoglycans, stimulate the release of glucose or free fatty acid by cells or gene expression, stimulate the release of proteoglycans, stimulate the release of proteoglycans, cells, inhibit the binding of A-peptide to factor VIIA, or detect the presence of tumour in a mammal. The nucleic acid and polypeptide encoded by it, are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, acquired immunodeficiency syndrome birth defects, premature aging, acquired immunodeficiency bybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. This is the amino acid sequence of a novel human secreted and
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Tumas D,
2000WO-US023522.
2000WO-US0330873.
2000WO-US0330873.
2000WO-US0332678.
2000WO-US034956.
2001WS-00796498.
2001WS-00796498.
2001WS-00808689.
2001US-00808689.
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2001US-00816744.
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2001US-00854280.
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ME, Goddard
Stewart TA,
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N-PSDB; ACD24025.
23 - AUG - 2000;

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14 - MAR - 2001;

15 - APR - 2001;

16 - MAY - 2001;

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18 - MAY - 2001;

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                       Length
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                      Score 3659.5; DB (Pred. No. 3.8e-205); Mismatches 45.
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                      ch 88.8%;
1 Similarity 87.0%;
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bone disorder; cartilage disorder; rheumatoid arthritis; obesity; sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia; hearis loss; coagulation disorder; stroke; heart attack; cardiant; antidiabetic; anorectic; vulnerary; antiarthritic; osteopathic; antirheumatic; auditory; cerebroprotective; angiogenic.
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New isolated PRO polypeptide useful for treating diabetes, rheumatoid
arthritis, sports injuries, obesity, hearing loss in mammals, stroke,
heart attack.
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L, Sherwood S
od WI, Zhang
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ski PJ, Gurney A
Watanabe CK, Wo
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A, Godowski
Tumas D, Wat
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98WO-US022991.
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98WO-US024855.
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99WO-US025108.
99WO-US025190.
99WO-US0205190.
99WO-US0205191.
99WO-US020514.
99WO-US028313.
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ME, Goddard Stewart TA,
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N-PSDB; ACA67166.
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Gerritsen ME,
Smith V, Stew
29-OCT-1998;
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10-MAR-1999;
11-MAY-1999;
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13-SEP-1999;
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15-SEP-1999;
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16-DEC-1999;
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18-PEB-2000;
18-PEB-2000;
19-FEB-2000;
19-FEB-2000;
19-FEB-2000;
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The present invention relates to the isolation of novel human PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides and polynucleotides are useful for preparing a medicament useful in the treatment of diabetes, bone and/or cartilage disorders (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity, hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting its expression in specific cells, tissues or cartural sources. ABU80870-ABU81144 represent the human PRO or natural sources invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at sequence.

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Sequence 723 AA;

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Score 3659.5; DB 6
Pred. No. 3.8e-205;
46; Mismatches 45;
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Query Match
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66318000 residues 478139 seqs, Searched:

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SUMMARIES

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Result No.	ğ		Length	DB	ID	Description
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US-08-083-590A-2 US-08-465-500-6 US-08-346-126-6 US-08-346-128-6 US-08-893-828-6 US-08-981-392-6 US-08-908-322-6 US-09-908-322-6 US-09-917-254-85 US-09-917-254-85 US-09-195-524-6 US-09-195-524-6 US-08-611-729A-6 US-09-195-524-6 US-08-611-729A-10 US-09-195-524-10 US-09-195-524-10
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ALIGNMENTS

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RESULT 1
US-08-981-392-12
US-08-981-392-12

Sequence 12, Application US/08981392

Fatent No. 6262025

APPLICANT: IBh-Horowicz, David

APPLICANT: IBh-Horowicz, David

APPLICANT: Lewis, Julian Hart

APPLICANT: Lewis, Julian Hart

APPLICANT: Artavanis-Tsakonas, Spyridon

APPLICANT: USA

CONFESSE: Pennie & Edmonds LLP

STATE: NY

COMPUTR: NY

COMPUTR: LOSA

ZIP: 10036/2711

COMPUTER: LOSA

COMPUTER: IBM Compatible

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COMPUTER: IBM Compatible

COMPUTR: LOSA

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Pred. No. 1.7e-301;
; Mismatches 0;
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SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,392
FILING DATE: 22-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-038
TELEPHONE: 212-790-9090
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEFX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
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Pred. No. 1.7e-301
0; Mismatches 0;
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FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-123
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/09/90
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/09/90
FILING DATE: 17-Jul-2001
CLASSIFICATION DATA:
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TYPE: amino acid

STRANDEDNESS: <Unknown>

HOPOLOGY: unknown

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NG
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AND METHODS
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Henrique, Domingos Ma
Lewis, Julian Hart
Artavanis-Tsakonas, S
Gray, Grace
F INVENTION: NUCLEOTIDE A
VERTEBRATE D
OF SEQUENCES: 94
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US-09-908-322-12
Sequence 12, Application US/09908322
Patent No. 6783956
GENERAL INFORMATION:
Henrique, Domingos M
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & EC
STREET: 1155 Avenue of
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
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                                   VSRCEHAPCHNGATCHORGORYMCECAQGYGGPNCOFLLPEPPPGPMVVDLSERHMESQG
                                                                                                                                                                                                                                             RDTKCQSQSLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVIAT
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CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,855
FILING DATE: 11-JUN-1997
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ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MAA-003.03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-7000
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US-08-872-855-5
; Sequence 5, Application US/08872855
; Patent No. 6121045
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean
APPLICANT: Gearing, David
; TITLE OF INVENTION: THERAPEUTIC US
; TITLE OF INVENTION: THERAPEUTIC US
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APPLICANT: Gearing, David
TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND
TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA

ZIP: 02109-2170

ZIP: 02109-2170

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,855
FILING DATE: 11-JUN-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
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Pred. No. 3.1e-290
4; Mismatches 16
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Post Office Square
                                                                                                                                                                                         Sequence 4, Application US/0887285
Patent No. 6121045
GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,
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Pred. No. 2e-2
11; Mismatches
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1 Similarity 93.4%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 713 amino acide
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
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US-09-068-740A-9
; Sequence 9, Application US/0; Patent No. 6337387
; GENERAL INFORMATION:
; APPLICANT: SAKANO, SEIJI
; APPLICANT: ITOH, AKIRA
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TYPE: an
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; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POI
; FILE REFERENCE: KP-8447
; CURRENT APPLICATION NUMBER: US/09/068,740A
; CURRENT FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: JP 7-299611
; PRIOR FILING DATE: 1995-11-17
; PRIOR FILING DATE: 1995-11-30
; PRIOR FILING DATE: 1996-11-15
; PRIOR FILING DATE: 1996-11-15
; RIOR FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Bapiens
US-09-068-740A-9
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Pred. No. 8e-2
46; Mismatches
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Best Local Similarity 87.0%;
Matches 630; Conservative
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No. 8e-267;
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Pred. No. 8e-206; Mismatches
RESULT 6
US-09-423-753-27
; Sequence 27, Application US/09423753
; Patent No. 6664098
; GENERAL INFORMATION:
; APPLICANT: SAKANO, SEIJI
; TITLE OF INVENTION: NOVEL DIFFERENTIATION IJ
; FILE REFERENCE: KP-8693
; CURRENT APPLICATION NUMBER: US/09/423,753
; CURRENT FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: PCT/JP98/02104
; PRIOR FILING DATE: 1998-05-13
; PRIOR FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 27
; SEQ ID NO 27
; LENGTH: 723
; LENGTH: 723
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al Similarity 87.0%;
630; Conservative
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; ORGANISM: Homo sapiens
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660 KRDTKCQPQGSSGEEKGTPTTLRGGEASERKRPDSGCSTSKDTKYQSVYVISEEKDECVI
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Pred. No. 8e-267;
5; Mismatches 45;
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APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Beresini, Maureen
APPLICANT: Desnoyers, Luc
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gaoweki, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: AND AND TRANSMEMBRA
TITLE OF INVENTION: SECRETED AND TRANSMEMBRA
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P33330R1C59
CURRENT APPLICATION NUMBER: US/10/140,002
                                                                                                                                                                                                                           Sequence 346, Application US/10140002
Patent No. 6725730
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
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Best Local Similarity 87.0%;
Matches 630; Conservative
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RLISRLTTORHLTVGEEWSQDLHSSGRTDLRYSYRFVCDEHYYGEGCSVFCRPRDDAFGH
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; Sequence 4, Application US/09068740A
; Patent No. 6337387.
; GENERAL INFORMATION:
; APPLICANT: SAKANO, SELJI
; APPLICANT: ITOH, AKIRA
; TITLE OF INVENTION:
; FILE REFERENCE: KP-8447
; CURRENT APPLICATION NUMBER: US/09/068,740A
; CURRENT FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: JP 7-299611
; PRIOR FILING DATE: 1995-11-17
; PRIOR FILING DATE: 1995-11-17
; PRIOR FILING DATE: 1995-11-17
; PRIOR FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin Ver: 2.1
; SEQ ID NO 4
; LENGTH: 702
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Pred. No. 3.2e-260;
15; Mismatches 43;
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; ORGANISM: Homo sapiens
US-09-068-740A-4
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Pred. No. 1e-264;
46; Mismatches
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; Sequence 6, Application US/09641612
; Patent No. 6703221
; GENERAL INFORMATION:
; APPLICANT: Vivien Chan et al.
; TITLE OF INVENTION: NOTCH RECEPTOR LIGANDS AN; FILE REFERENCE: PPO-1602.002 / 200130.498
; CURRENT APPLICATION NUMBER: US/09/641,612
; CURRENT FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 86.5%;
Matches 626; Conservative
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US-09-908-322-2
; Sequence 2, Application US/0950cc.
; Patent No. 6783956
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
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Pred. No. 6.5e
3; Mismatches
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                                                                   Query Match
Best Local Similarity 78.5%;
Matches 574; Conservative
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                                unknown
LENGTH: 728 & TYPE: amino & STRANDEDNESS: TOPOLOGY: un}
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        GCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCRNGATCTNTGQGSYTCSCRPGYT
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                                               SDNPDGGYTCHCPLGFSGFNCEKKMDLCGSSPCSNGAKCVDLGNSYLCRCQAG
                                                                                                                            722
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                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08981392
; Sequence 2, Application US/08981392
; Patent No. 6262025
; GENERAL INFORMATION:
    APPLICANT: Ish-Horowicz, David
    APPLICANT: Henrique, Domingos Manuel Pinto
    APPLICANT: Henrique, Domingos Manuel Pinto
    APPLICANT: Lewis, Julian Hart
    APPLICANT: Artavanis-Tsakonas, Spyridon
    APPLICANT: Artavanis-Tsakonas, Spyridon
    APPLICANT: Gray, Grace
    TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN
    TITLE OF INVENTION: OF VERTEBRATE DELTA GE
    NUMBER OF SEQUENCES: 94
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Pennie & Edmonds LLP
    STREET: 1155 Avenue of the Americas
    CITY: New York
    STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 22-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-038
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-869-8864
TELEFX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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22-DEC-1997
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ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/90
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US-08-981-392-2
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             YTGKNCSAPVSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDL
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 PCSNGAKCVDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFS:
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                                                                                                                                                                                                                                                                                                                                                                  ritle of invention: novel human delta3 compositions and number of sequences: 23 correspondence address: 23 Addressee: Foley, Hoag & Eliot Llp STREET: One Post Office Square CITY: Boston
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Pred. No. 4e-244
73; Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,855
FILING DATE: 11-JUN-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MAA-003.02
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08872855
Patent No. 6121045
GENERAL INFORMATION:
APPLICANT: McCarthy, Sean
APPLICANT: Gearing, David
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4; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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US-08-872-855-8
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Best Local Sim
Matches 574;
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STATE: M
COUNTRY:
ZIP: 021
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Best Local Similarity 78.5%; Pred. No. 6.5e-245;
Matches 574; Conservative 73; Mismatches 72;
                                                                                                                                                                     COMPUTER: 15M COMPACIDIE

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/908,322

FILING DATE: 17-Jul-2001

CLASSIFICATION ATA:

APPLICATION NUMBER: 08/981,392

FILING DATE: 22-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 7326-123

TELEPHONE: 212-790-9090

TELEPHONE: 212-790-9090

TELEFAX: 212-869-8864

TELEFAX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:
                                                              Edmonds LLP
of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-908-322-2
                                                                                                        COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
Gray, Grace
INVENTION: NUCLEOTIDE
VERTEBRATE
                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 728 amino acids
TYPE: amino acid
                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & E
STREET: 1155 Avenue o
CITY: New York
STATE: NY
COUNTRY: USA
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e-230;
87;
                                                                                                                                                                                                   Score 3167.5; Fred. No. 7.5e 89; Mismatches
                                   392
                                                                                    -03
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,39
FILING DATE: 22-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-03
TELEFHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 amino acids
TYPE: amino acid
                                JMBER: US/08/981,
22-DEC-1997
                                                                                                                                                                                                   76.9%;
ilarity 72.9%;
Conservative 8
                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                     unknown
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                                                                                                                                                                                                            11 Similarity
534; Conser
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                CACRTFFRVCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGA-GIDPAFS
                                                 GFTWPGTFSLIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHS
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US-08-981-392-5
Sequence 5, Application US/08981392
SEPPLICANT: Ish-Horowicz, David
APPLICANT: Henrique, Domingos Manuel
APPLICANT: Henrique, Domingos Manuel
APPLICANT: Artavanis-Tsakonas, Spyrid
APPLICANT: Artavanis-Tsakonas, Spyrid
APPLICANT: Gray, Grace
TITLE OF INVENTION: OF VERTEBRATE DELT
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & T
STREET: 1155
CITY: N
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ZIP: 10036/2711
COMPUTER READABLE
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ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Versi
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,855
FILING DATE: 11-JUN-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MAA-003.02
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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US-08-872-855-7
Sequence 7, Application US/08872855
Fatent No. 6121045
GENERAL INFORMATION:
APPLICANT: McCarthy, Sean
APPLICANT: Gearing, David
TITLE OF INVENTION: THERAPEUTIC US
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
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INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
VERTEBRATE DELTA GENE AND METHODS BASED
-RRRPDSAYSTSKDTKY
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                                                                                                                                                                                                                                                                                 Manuel Pinto
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ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                       Spyridon
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BER: 7326-123
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,323
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-12
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
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                                                                                                                                                                                                Sequence 5, Application US/09908322
Patent No. 6783956
GENERAL INFORMATION:
APPLICANT: ISh-Horowicz, David
Henrique, Domingos lewis, Julian Hart
Artavanis-Tsakonas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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TYPE: amino acid
STRANDEDNESS: <Unknown:
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MEDIUM TYPE: Diskette
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
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10036/2711
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                                                                                                                                                              RESULT 14
US-09-908-322-5
                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER
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                                                            Score 3161.5; DB 3
Pred. No. 2.1e-229;
); Mismatches 88;
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TELEFAX: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 amino acids
TYPE: amino acids
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                                                            Query Match
Best Local Similarity 72.7%;
Matches 533; Conservative
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US-09-783-931-12 4121 Title: Perfect

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residues 1575965 segs, 354694765 Searched

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SUMMARIES

Sequence 12, Appl Sequence 12, Appl Sequence 107, App Sequence 4, Appli Sequence 108, App Sequence 5, Appli Sequence 5, Appli Sequence 316, App Sequence 346, App Sequence 346, App Sequence 346, App Sequence 346, App ion Descript US-09-908-322-12 US-09-908-322-12 US-10-042-865-107 US-10-731-741-4 US-10-417-719-4 US-10-417-719-4 US-10-417-719-5 US-09-828-366-21 US-09-995-593A-9 US-09-995-593A-9 US-09-995-593A-9 US-10-140-808-346 US-10-123-904-346 ü 8 D Length Query Match 00444400000000 97 4121 4003 4003 3971 3848 3659.5 3659.5 3659.5 3659.5 core ഗ Result No. 126456788015E

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ALIGNMENTS

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Gray, Grace
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
VERTEBRATE DELTA GENE AND METHODS BASED THEREON
                                                                                   Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
Gray, Grace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-123
                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
RESULT 1
US-09-908-322-12
; Sequence 12, Application US/09908322
; Patent No. US20020107194A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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COUNTRY: USA
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TELEPHONE: 212-790-9090
TELEX: 66141 PENNIE
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Best Local Similarity 100.0%;
Matches 722; Conservative (
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RESULT 2 US-09-783-931-12

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Pred. No. 4.3e-272;
Mismatches 0;
                                                                                                                VERTEBRATE
                                                                                                                                                                                                                                                                              COMPUTER: DIBRECTE
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/783,931
FILING DATE: 15-Feb-2001
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-122
TELEPHONE: 212-790-9090
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
                                                                                                                                                                                     Americas
                                                                                    Spyridon
                                        Ish-Horowicz, David
Henrique, Domingos Manuel
Lewis, Julian Hart
Artavanis-Tsakonas, Spyric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown;

MOLECULE TYPE: protein;

SEQUENCE DESCRIPTION: SEQ ID NO: 12
US-09-783-931-12
                                                                                        Gray, Grace
INVENTION: ANTIBODIES TO
AND FRAGMENTS
                                                                                                                                                                      Edmonds
of the A
Sequence 12, Application US/09783931
Publication No. US20030073620A1
GENERAL INFORMATION:
APPLICANT: ISh-Horowicz, Davi
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TYPE: amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & E
STREET: 1155 Avenue o
CITY: New York
STATE: NY
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Local Similarity 100.0%;
nes 722; Conservative (
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Query Match
Best Local Similarity 97.2%;
Matches 702; Conservative
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-10-042-865-107
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RDTKCQSQSLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVIAT
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                                                               DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYT
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CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/260,417
PRIOR FILING DATE: 2001-01-09
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Carhusen, Furest APPLICANT: Casman, Stacie J
APPLICANT: Casman, Stacie J
APPLICANT: Shenoy, Suresh G
APPLICANT: Shenoy, Suresh G
APPLICANT: Spytek, Kimberly
APPLICANT: Spytek, Kimberly
APPLICANT: Cangolli, Esha A
APPLICANT: Gangolli, Esha A
APPLICANT: Patturajan, Meera
APPLICANT: Patturajan, Meera
APPLICANT: Patturajan, Meera
APPLICANT: Tchernev, Velizar T
APPLICANT: Taylor, Sarah
APPLICANT: Gloo, Xiaojia
APPLICANT: Gloo, Xiaojia
APPLICANT: Grosse, William M
APPLICANT: Grosse, William M
APPLICANT: Edinger, Shlomit R
APPLICANT: Edinger, Shlomit R
APPLICANT: Edinger, Shlomit R
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M
APPLICANT: Malyankar, Uriel M
APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: Stone, David
TITLE OF INVENTION: Using the Same
TITLE OF INVENTION: WINDER
                                                                                                                                                                                                                                                                                                          S-10-042-865-107
Sequence 107, Application US/10042865
Publication No. US20040029216A1
GENERAL INFORMATION:
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: Li, Li
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Pred. No. 4.6e-264
; Mismatches 16
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PRIOR APPLICATION NUMBER: 60/260,83
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: 60/272,33
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 264
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 107
LENGTH: 722
TYPE: PRT
ORGANISM: Mus musculus
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Pred. No. 6.9e-262
4; Mismatches 16
                                                                                                                                        THEREOF
                                                                          Sequence 4, Application US/10417719

Publication No. US20030180784A1

GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: McCarthy, Sean
APPLICANT: Gearing, David
TITLE OF INVENTION: HUMAN DELTA3 AND USES 7
FILE REFERENCE: MBIO1997-002CP2M
CURRENT APPLICATION NUMBER: US/10/417,719
CURRENT FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: US/09/568,218
PRIOR FILING DATE: 1997-06-11
PRIOR FILING DATE: 1997-06-11
PRIOR FILING DATE: 1997-04-04
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 97.0%;
Matches 700; Conservative
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LENGTH: 720
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US-10-417-719
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           Sequence 4, Application US/10731741

Sequence 4, Application US/10731741

Publication No. US20040171148A1

GENERAL INFORMATION:

APPLICANT: Schmitt, Thomas M.

APPLICANT: Zuniga-Pflucker, Juan-Carlos

TITLE OF INVENTION: Cell Preparations Comprising Cells of

TITLE OF INVENTION: Lineage and Methods of Making and Usi

FILE REFERENCE: 2223-171

CURRENT APPLICATION NUMBER: US/10/731,741

CURRENT FILING DATE: 2003-12-10

PRIOR APPLICATION NUMBER: 60/432,525

PRIOR FILING DATE: 2002-12-10

NUMBER OF SEQ ID NOS: 50

SOFTWARE: PatentIn version 3.1

SEQ ID NO 4
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1.6e-264;
les 16;
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Best Local Similarity 97.2%;
Matches 702; Conservative
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                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-731-741-4
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RESULT 4
US-10-731-741-4
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US-10-417-719-5
; Sequence 5, Application US/10417719
; Publication No. US20030180784A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: McCarthy, Sean
; APPLICANT: Gearing, David
; TITLE OF INVENTION: HUMAN DELTA3 AND USES T
; FILE REFERENCE: MBIO1997-002CP2M
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US/09/568,218
; PRIOR FILING DATE: 2000-05-09
; PRIOR FILING DATE: 1997-06-11
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Polynucleotides Encoding Them and
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APPLICANT: Guo, Xiaojia
APPLICANT: Goose, William M
APPLICANT: Grosse, William M
APPLICANT: Grosse, William M
APPLICANT: Gerlach, Valerie L
APPLICANT: Gerlach, Valerie L
APPLICANT: Edinger, Shlomit R
APPLICANT: Edinger, Shlomit R
APPLICANT: Blerman, Karen
APPLICANT: Blerman, Karen
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Smithson, Glennda
APPLICANT: Stone, David
TITLE OF INVENTION: Using the Same
FILE REFERENCE: 21402-537
CURRENT FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-04-18
                                                                                                                                                                                    Sequence 108, Application US/10042865
Publication No. US20040029216A1
GENERAL INFORMATION:
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Casman, Stacie J
Shenoy, Suresh G
Spytek, Kimberly
Zhong, Mei
Gangolli, Esha A
Burgess, Catherine E
Patturajan, Meera
Vernet, Corine A.M
                                                                                                                                                                                                                                                                                                                                                               Tchernev, Velizar
Miller, Charles E
Guo, Xiaojia
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US-10-042-865-108
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Pred. No. 1.1e
16; Mismatches
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APPLICANT: Ashkenazi, Avi
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Klein, Robert D.
APPLICANT: Napier, Mary
APPLICANT: Wood, William I.
APPLICANT: Yuan, Jean
TITLE OF INVENTION: METHODS AND COMPOSIT
TITLE OF INVENTION: CELL GROWTH
FILE REFERENCE: P1694R1C1
CURRENT APPLICATION NUMBER: US/09/828,36
CURRENT FILING DATE: 2001-04-05
Prior filing data removed - refer to PAL
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 21
LENGTH: 723
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Best Local Similarity 87.0%;
Matches 630; Conservative 4
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Pred. No. 5.2e-253;
11; Mismatches 28;
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US-09-828-366-21
; Sequence 21, Application US/0982836(
; Patent No. US20020010137A1; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
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   83
  PRIOR APPLICATION NUMBER: 08/83;
PRIOR FILING DATE: 1997-04-04;
NUMBER OF SEQ ID NOS: 52;
SOFTWARE: FastSEQ for Windows V;
SEQ ID NO 5;
LENGTH: 713
                                                                          93.2%;
ilarity 93.4%;
Conservative 1:
                                             TYPE: PRT
ORGANISM: Rattus No
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Sequence 9, Application US/09995593A

Patent No. US20020128197A1

GENERAL INFORMATION:

APPLICANT: SAKANO, SELJI

APPLICANT: TOH, AKIRA

TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE

FILE REFERENCE: KP8447DIV

CURRENT APPLICATION NUMBER: US/09/995,593A

CURRENT FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: 09/068,740

PRIOR FILING DATE: 1998-06-18

PRIOR FILING DATE: 1998-11-17

PRIOR FILING DATE: 1995-11-17

PRIOR FILING DATE: 1995-11-17

PRIOR FILING DATE: 1995-11-17

PRIOR FILING DATE: 1996-11-15

NUMBER OF SEQ ID NOS: 48

SOFTWARE: Patentin Ver. 2.1
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Pred. No. 1.1e-240;
5; Mismatches 45;
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Local Similarity 87.0%;
hes 630; Conservative
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ID NO 9
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                                              KDVSVSIIGATQIKNTNKKADFHGDHGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHS
                                                                                                                                                     APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Chang
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT APPLICATION NUMBER: 60/049911
PRIOR APPLICATION NUMBER: 60/049911
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 346, Application US/10028072
Publication No. US20030004311A1
GENERAL INFORMATION:
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1997-10-17
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FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/062816
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Beresini, Maureen
DeForge, Laura
Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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APPLICATION NUMBER:
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PRIOR APPLICATION NUMBER: 60/081819
PRIOR PLING DATE: 1998-604-28
PRIOR PLING DATE: 1998-604-29
PRIOR PLING DATE: 1998-604-29
PRIOR PLING DATE: 1998-604-29
PRIOR PLING DATE: 1998-604-29
PRIOR PLING DATE: 1998-60-607
PRIOR PLING DATE: 1998-60-13
PRIOR PLING DATE: 1998-60-17
PRIOR PLING DATE: 1998-60-19
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Query Match

88.8%; Score 3659.5; DB

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Pred. No. 1.1e-240;
; Mismatches 45;
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POI
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C182
CURRENT APPLICATION NUMBER: US/10/140,808
CURRENT APPLICATION NUMBER: US/10/140,808
Prior Apploication removed - See File Wrapper or I
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 346
LENGTH: 723
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 Pred. No. 1.1e-240;
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Publication No. US20030017563A1
GENERAL INFORMATION:
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
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Conservative
 l Similarity
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Sequence 346, Application US/10123904
Publication No. US20030022328A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
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Best Local Similarity 87.0%;
Matches 630; Conservative
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; ORGANISM: Homo Sapien
US-10-123-904-346
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                                                                                                                GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Beresini, Maureen
APPLICANT: Desnoyers, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary E.
APPLICANT: Godard, Audrey
APPLICANT: Godard, Audrey
APPLICANT: Godard, Audrey
APPLICANT: Godard, Audrey
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timethy A.
APPLICANT: Stewart, Timethy A.
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Watanabe, Colin K
APPLICANT: Pumas, Daniel
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APPLICANT:
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Pred. No. 1.1e-240;
46; Mismatches 45;
                                                                       Application US/10121049
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US-10-121-049-346
                                                                    Sequence 346, Applic
Publication No. US20
GENERAL INFORMATION:
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Pred. No. 1.1e-240;
6; Mismatches 45; ]
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APPLICANT: Beresini, Maureen
APPLICANT: Beresini, Maureen
APPLICANT: Berose, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Sherwood, Steven
APPLICANT: Shower, Timothy A.
APPLICANT: Shower, Timothy A.
APPLICANT: Shang, Zemin
APPLICANT: Thans, Daniel
APPLICANT: Abang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POL
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C54
CURRENT APPLICATION NUMBER: US/10/123, 904
CURRENT FILING DATE: 2002-04-16
Prior Application removed - See File Wrapper or Pa
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 346
LENGTH: 723
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Sequence 346, Application US/10140470

Fublication No. US20030022331A1

GENERAL INFORMATION:

APPLICANT: Beresini, Maureen

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gaowski, Paul J.

APPLICANT: Godowski, Paul J.

APPLICANT: Sherwood, Steven

APPLICANT: Tumas, Daniel

APPLICANT: Tumas, Daniel

APPLICANT: Abang, Zemin

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3330RIC160

CURRENT APPLICATION NUMBER: US/10/140, 470

CURRENT APPLICATION NUMBER: US/10/140, 470

CURRENT APPLICATION NUMBER: US/10/140, 470

CURRENT APPLICATION NUMBER: US/10/140, 470
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NUMBER OF SEQ ID NOS: 550
EQ ID NO 346
LENGTH: 723
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ORGANISM: Homo Sapien
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US-10-175-746-346
; Sequence 346, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddwski, Paul J.
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; Pred. No. 1.1e-240;
46; Mismatches 45;
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POI
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C353
CURRENT APPLICATION NUMBER: US/10/175,746
CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or Pi
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 346
LENGTH: 723
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Best Local Similarity 87.0%;
Matches 630; Conservative
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US-09-783-931-12 4121 score: Title: Perfect

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283416 segs, 96216763 residues Searched

283416 Total number of hits satisfying chosen parameters

length: 0 length: 2000000000 eeq eeq Minimum DB Maximum DB Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR Database

R_79:* pir1:* pir2:* pir3:* 4 6 6 4

Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being gand is derived by analysis of the total score distribution.

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ALIGNMENTS

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PID:98065
DELTA-like 1 - mouse

C; Species: Mus musculus (house mouse)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C; Accession: 148324
A; Reference number: 148324; MUID: 95401858; PMID: 7671806
A; Reference number: 148324
A; Reference number: 148324
A; Reference number: 148324
A; Residues: 1-722 < RES>
A; Residues: 1-722 < RES>
A; Residues: 1-722 < RES>
A; Cross-references: UNIPROT: Q61483; EMBL: X80903; NID: g806569; PIDN: CAA56865.1; PID: A; Gene: D11
C; Superfamily: delta-4 protein; EGF homology < EGF2>
F; 331-362/Domain: EGF homology < EGF2>
F; 446-477/Domain: EGF homology < EGF>
F; 484-515/Domain: EGF homology < EGF>
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ö Gape .. 0 722; Indela Length Query Match
97.1%; Score 4003; DB 2;
Best Local Similarity 97.2%; Pred. No. 1.1e-240
Matches 702; Conservative 4; Mismatches 16 4 ;

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VCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCGSSPCSNGAKCV

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ATVRDTHSKRDTKCQSQSLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSA
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JC7570
Delta-4 protein - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-C;Accession: JC7570
C;Accession: JC7570
R;Yoneya, T.; Tahara, T.; Nagao, K.; Yamada, Y.; Yamamoto, T.; Osawa, N.; Biochem. 129, 27-34, 2001
A;Title: Molecular cloning of Delta-4, a new mouse and human notch ligs A;Reference number: JC7569; MUID: 21064937; PMID:11134954
A;Residues: JC7570
A;Residues: I-685 «YON»
A;Residues: L-685 «YON»
A;Residues: L-685 «YON»
A;Residues: UNIPROT:09NR61; DDBJ:AB043894
C;Comment: This protein, a member of the Notch family of proteins, is a ates the Notch signaling, the growth or differentiation of vascular ence; Genetics:
A;Gene: delta-4
C;Superfamily: delta-4 protein; EGF homology
C;Keywords: transmembrane protein
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99; Mismatches 190;
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150719
C-Delta-1 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2(C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2(C;Accession: 150719
R;Henrique, D.; Adam, J.; Myat, A.; Chitnis, A.; Lewis, J.; Ish-Horowicz, Nature 375, 787-790, 1995
A;Title: Expression of a Delta homologue in prospective neurons in the cl A;Reference number: 150719; MUID: 95319507; PMID: 7596411
A;Reference number: 150719; MUID: 95319507; PMID: 7596411
A;Residues: 1-728 <HEN>
A;Residues: 1-728 <HEN>
A;Residues: UNIPROT: Q90656; EMBL: U26590; NID: 9882411; PIDN: AACE9(C;Superfamily: delta-4 protein; EGF homology <EGF1>
F;299-332/Domain: EGF homology <EGF2>
F;339-370/Domain: EGF homology <EGF2>
F;46-447/Domain: EGF homology <EGF2>
F;454-485/Domain: EGF homology <EGF>
F;492-523/Domain: EGF homology <EGF>
F;492-523/Domain: EGF homology <EGF>
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Qy 232 QHGYCDKPGECKCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYC 291 Db 229 QNGYCSKPAECLCRPGWQGRLCNECIPHNGCRHGTCSTPWQCTCDEGWGGLFCDQDLNYC 288 Qy 292 THHKPCRNGATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSC 351 Db 289 THHSPCKNGATCSNSGQRSYTCTCRPGYTGANCELELSECDSNPCRNGGSCKDQEDGYHC 348 Qy 352 TCPPGFYGKVCELSAMTCADGPCFNGGRCSD-NPDGGYTCHCPLGFSGFNCEKKMDLCGS 410 Db 349 LCPPGYYGLHCEHSTLSCADSPCFNGGSCRERNQGANYACECPPNFTGSNCEKKVDRCTS 408	411 SPCSNGAKCVDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPP : : :		Qy 645 RDLKGDEATVRDTHSKRDTKCOSQSLQEKRRSPQHLGVGRFLTENRPESVY 695 Db	RESULT 4 Jordes Mus musculus (house mouse) Delta-4 protein - mouse C.Species: Mus musculus (house mouse) C.Species: Mus musculus (house mouse) C.Species: Jo-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004 C.Accession: JC7569 R.Yoneya, T.; Tahara, T.; Nagao, K.; Yamada, Y.; Yamamoto, T.; Osawa, M.; Miyatani, S.; J. Biochem. 129: 27-34, 2001 A.;Hitle: Molacular cloning of Delta-4, a new mouse and human notch ligand. A.;Recreace number: JC7569; MUDD: 21064937; PMID:11134954 A.;Recreace number: JC7569; MUDD: 21064937; PMID:11134954 A.;Residues: JC666 * KNOS A.;Coss-reference unimper: JC7569; MUDD: 21064937; PMID:11134954 A.;Residues: JC666 * KNOS A.;Coss-reference unimper: JC7569; MUDD: 21064937; PMID:11134954 A.;Residues: JC666 * KNOS A.;Coss-reference unimper: JC7569; MUDD: 21064937; PMID:11134954 A.;Gene: Gelta-4 C.;Coment: This protein, a member of the Notch family of proteins, is a transmembrane reates the Notch signaling, the growth or differentiation of vascular endothelial cells. C.;Generics: C.;Generics: A.;Gene: delta-4 C.;Superfamily: delta-4 protein; BGF homology Query Match A.;Gene: delta-4 C.;Superfamily: delta-4 C.;Cenervative: delta-4

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melanogaster)
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NiAlternate names: gene Di protein
NiAlternate names: gene Di protein
Cispecias: Drosophila melanogaster
Cispecias: Drosophila melanogaster is expressed in
Rivaessin, H.; Bremer, K.A.; Knust, E.; Campos-Ortega, J.A.
EMBO J. 6, 341-340, 1987
A;Title: The neurogenic gene Delta of Drosophila melanogaster is expressed in
A;Reference number: S00670
A;Accession: S00670
A;Accession: S00670
A;Accession: B00 < vAE>
A;Cross-references: UNIPROT: P10041; EMBL: X06289; NID:g7852; PID:g7853
R;Knust, E.; Dietrich, U.; Tepass, U.; Bremer, K.A.; Weigel, D.; Vaessin, H.;
EMBO J. 6, 761-766, 1987
A;Title: EGF homologous sequences encoded in the genome of Drosophila melanoge
A;Accession: A26637
A;Accession: A26637
A;Accession: A26637
A;Accession: A26637
A;Accession: A26637
A;Cross-references: GB:X05140; NID:g7851; PIDN:CAA28786.1; PID:g929563
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spnpcinggscopsgkcicpsgfsgtrcetniddclghocenggtcidmvnoyrcocvpg
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                                                 VCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGAGI-DPAFSNPIRFPFGFTWPGTF
                                                                  SLIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFVCD
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                                                                                                                                                                                                                                                                                      - ACVVFCMKRKRKRAQEKDDAEARKQNEQNAVATM
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VCLKHYQATIDTTSQCTYGDVITPILGENSVNLTDAQRFQNKGFTNPIQFPFSFSWPGTF
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A31246
neurogenic protein Delta precursor - fruit fly (Drosophila melanogaster)
C; Species: Drosophila melanogaster
C; Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 02-Aug-2
C; Accession: A31246
R; Kopczynski, C.C.; Alton, A.K.; Fechtel, K.; Kooh, P.J.; Muskavitch, M.; Genes Dev. 2, 1723-1735, 1988
A; Title: Delta, a Drosophila neurogenic gene, is transcriptionally compla, R; Réference number: A31246; MUID:89196890; PMID:3149249
A; Reference number: A31246; MUID:89196890; PMID:3149249
A; Residues: 1-832 < KOP>
A; Cross-references: GB:Y00222
C; Genetics:
A; Cross-references: FlyBase:FBgn0000463
C; Superfamily: neurogenic protein delta; EGF homology < EGF1>
F; 295-328/Domain: EGF homology < EGF1>
F; 422-450/Domain: EGF homology < EGF3>
F; 533-564/Domain: EGF homology < EGF3>
                                                                                      CMNRVNSFECVCANGFRGKQCD----EESYDSVTFDAHQYGATTQARADGLTN
    VCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGAGI-DPAFSNPIRFPFGF
                                                                    LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYS
                                                                                                                                    EHYYGEGCSVFCRPRDDAFGHFTCGDRGEKMCDPGWKGQYCTDPICLPGCDDQH
                                                                                                                                                                                                                                                                    GATCTNTGQGSYTCSCRPGYTGANCELEVDECAP -- SPCKNGASCTD -- - LEDS
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Pred. No. 2.6e-83;
95; Mismatches 240;
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locus delta protein #status
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_
C;Accession: A56136
R;Lindsell, C.E.; Shawber, C.J.; Boulter, J.; Weinmaster,
Cell 80, 909-917, 1995
A;Title: Jagged: a mammalian ligand that activates Notchl
A;Reference number: A56136; MUID:95211842; PMID:7697721
A;Accession: A56136
                                                                                                                  -83;
240;
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A; Cross-references: FlyBase: FBgn0000463
C; Superfamily: neurogenic protein delta; EGF homology
C; Keywords: transmembrane protein
F;1-18/Domain: signal sequence #status predicted <SIG
F;19-88/Product: neurogenic repetitive locus delta pr
F;457-488/Domain: EGF homology <EGF1>
F;533-564/Domain: EGF homology <EGF2>
                                                                                                    Score 1463.5; DB
Pred. No. 2.7e-83;
95; Mismatches 24(
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                                                                                                          Length
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                                                                                                                           .74;
215;
                                                                                                          31.8%; Score 1312; DB 2 40.6%; Pred. No. 8.8e-74
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                                                                                                                          ed. No. 8.8 Mismatches
                                              <EGF1><EGF2><EGF2>
                                                                                                                                      78;
A; Molecule type: mRNA
A; Residues: 1-1220 <LIN>
A; Cross-references: GB:L38483
F; 379-410/Domain: EGF homology <
F; 492-523/Domain: EGF homology <
F; 634-665/Domain: EGF homology <
                                                                                                                         Local Similarity 40.6 tes 239; Conservative
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Pred. No. 2.1e-42;
1; Mismatches 196;
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pecies: Xenopus laevis (African clawed frog)
ate: 12-Oct-1990 #sequence_revision 12-Oct-1990
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QDLNFCGTHEPCKHGGTCENTAPDKYRCTCAEGLSGEQCEIVEHPCATRPCRNGGTCTLK
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8/Domain: intracellular #status predicted <INT>
247,331,412,452,558,739,965,977,1004,1030,1150/Binding
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C; Keywords: glycoprotein; transmembrane protein
C; Keywords: glycoprotein; transmembrane protein
F; 1-84/Domain: signal sequence #status predicted <SIG>F; 1-84/Domain: signal sequence #status predicted <MAF; 85-1221/Domain: extracellular #status predicted <EXT>F; 85-1221/Domain: EGF homology <EG01>F; 283-316/Domain: EGF homology <EG02>F; 319-348/Domain: EGF homology <EG03>F; 355-388/Domain: EGF homology <EG05>F; 355-488/Domain: EGF homology <EG05>F; 615-645/Domain: EGF homology <EG08>F; 652-683/Domain: EGF homology <EG09>F; 652-683/Domain: EGF homology <EG09>F; 650-720/Domain: EGF homology <EG19>F; 641-876/Domain: EGF homology <EG11>F; 883-914/Domain: EGF homology <EG12>F; 883-914/Domain: EGF homology <EG13>F; 883-914/Domain: EGF homology <
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             Fleming, R.J.; Scottgale, T.N.; Diederich, R.J.; Artavenes Dev. 4, 2188-2201, 1990; Title: The gene Serrate encodes a putative EGF-like triperence number: A36666; MUID:91099666; PMID:2125287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - ASVSPEPPCTYGSAVTPVLGVDS
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Pred. No. 1.9e-62;
; Mismatches 197;
                                                                                                                                                                                                                                    PID:9158
R;Fleming, R.J.; Scottgale, T.N.; Diederich, Genes Dev. 4, 2188-2201, 1990
A;Title: The gene Serrate encodes a putative A;Reference number: A3666; MUID:91099666; PM A;Accession: A3666
A;Accession: A3666
A;Cross-references: GB:M35759; NID:g158605; PM Cross-references: GB:M35759; NID:g158605; PM Cross-references: GB:M35759; NID:g158605; PM Cross-references: FlyBase:FBgm0004197
C;Genetics: A;Cross-references: FlyBase:FBgm0004197
C;Genetics: A;Genetics: FlyBase:FBgm0004197
F;85-1408/Domain: EGF homology cEG02>
F;395-488/Domain: EGF homology cEG03>
F;690-7000main: EGF homology cEG12>
F;690-7000main: EGF homology cEG13>
F;81-952/Domain: EGF homology cEG13>
F;81-952/Domain: EGF homology cEG13>
F;81-952/Domain: EGF homology cEG14>
F;921-106/Region: cysteine-rich
F;122-1246/Domain: transmembrane #status pre
F;122-1246/Domain: intracellular #status pre
F;122-1246/Domain: intracellular #status pre
F;122-1246/Domain: intracellular #status pre
F;152,196;247,331,412,452,558,739,965,977,100
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Local Similarity 33.0%;
nes 226; Conservative
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F;416-449/Domain: EGF homology <egg93> F;435-487/Domain: EGF homology <egg04> F;494-552/Domain: EGF homology <egg05> F;323-563/Domain: EGF homology <egg05> F;607-638/Domain: EGF homology <egg05> F;607-638/Domain: EGF homology <egg05> F;755-788/Domain: EGF homology <egg15> F;755-826/Domain: EGF homology <egg15> F;755-826/Domain: EGF homology <egg15> F;795-929-90/Domain: EGF homology <egg15> F;795-9104/Domain: EGF homology <egg15> F;103-1018/Domain: EGF homology <egg15> F;103-1018/Domain: EGF homology <egg15> F;103-1018/Domain: EGF homology <egg16> F;1149-1180/Domain: EGF homology <egg18> F;1149-1180/Domain: EGF homology <egg18> F;1131-1245/Domain: EGF homology <egg18> F;1131-1255/Domain: EGF homology <egg18> F;1131-1255/Domai</egg18></egg18></egg18></egg18></egg18></egg18></egg18></egg18></egg18></egg18></egg18></egg18></egg18></egg18></egg18></egg18></egg18></egg18></egg18></egg18></egg18></egg18></egg18></egg18></egg18></egg18></egg18></egg18></egg18></egg18></egg18></egg18></egg18></egg18></egg18></egg18></egg16></egg15></egg15></egg15></egg15></egg15></egg15></egg15></egg05></egg05></egg05></egg05></egg04></egg93>	33 ATENPERLISTUTTORHITYGEEWSODLHSSGRTDLRYSYRFVCDEHYYGEGGSV
B75 -NF 353 CPF 933 CPF 413 CSN 413 CSN 473 TGF 473 TGF 473 TGF 473 TGF 473 TGF 1052 TGI 1053 TGI 1054 TGI 1055 T	ession: S25 ecule type: idues: 1551 ss-referenc delli, M.; Cell Res. 2 le: Motch A erence numb ession: C49 tus: prelim ecule type: idues: 1161 ss-referenc erimental s e: sequence an, R.; Wei ll Biol. 12 le: Mouse n erence numb ecule type: idues: prelim ecule type: idues: This ecule type: erence numb ecule type: cerimental s erence numb ecule type: idues: This eriment: This erics: - 136/Domain -175/Domain -254/Domain

ò	55/ DEDECARVOCVREKEÇKEÇKEÇERIETMNEANCÜREKDVSVSIIGATÜLKNIN 616	<u></u>	
QQ	1130YCHCQAGYTGSYCEDEVDECSPNPCQNGATCTDYLGGFSCKCV- 1172	qa	949 CATNPCQNGANCTDCVD-SYTCT
ò	617 KKADFHGDHGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTH 658	ò	Q,
qq	1173 AGYHGSNCSEEINECLSQPCQNGGTCIDLTNSYKCSCPRGTQGVHCEINVDDCHPPLD 1230	ପ୍ପ	1008 LCPPGFTGSYCQYDVNECDSRP
ò	659 -SKRDTKC 665	ò	489 CHNGATCHORGORYMCECAOGYG
qq	: 1231 PASRSPKC 1238	q	1068 CKNGGKCWQTNTQYHCECRSGWI
		ò	534 RHMESQGGPFPWVAVCAGVVLVI
S18188	\$ (Cuch	qa	1128 KH
C;Specie	ttus norvegicus (Norway rat)	γ̈́ο	594 ANCQREKDVSVSIIGATQIKNTN
C;Date: C;Access	D-1994 #sequence_revision S18188	q	1158 ATCTDYLGGFSCKCV
R,Weinma Developm	G.; Roberts, V.J.; Lemke, G. 13, 199-205, 1991	ò	651EATVRDIH
A; Title: A ho A; Reference n	OF TO	qa	
A; Access A; Molecu	818 De:		
A; Residu	-2531 <wei> ences: EMBL:X57405: NID:q57634: PID:</wei>	RESULT A40136	F 13
C, Superf	notch protein; ankyrin repeat homology;	ibro	ellin Ia - sea urchin (St
F;987-10 F;1025-1	main: EGF homology <egf1 omain: EGF homology <egf< td=""><td>N;Alte N;Cont</td><td>ernate names: epidermal c cains: alternatively spli</td></egf<></egf1 	N;Alte N;Cont	ernate names: epidermal c cains: alternatively spli
F;1233-1	omain: EGF homology <egf2></egf2>	C;Spec	dies: Strongylocentrotus
F;19171	omain: ankyrin repeat homology <anz< td=""><td>C; Bace</td><td>assion: A40136; B40136; C401</td></anz<>	C; Bace	assion: A40136; B40136; C401
F; 1984-7 F; 2017-2	omain: ankyrin repeat nomology omain: ankyrin repeat homology	K;Deig J. Mol	gadiilo-keynoso, m.G.; koilo, [. Evol. 29. 314-327, 1989
F;2050-2	omain: ankyrin repeat homology <an5< td=""><td>A;Tit]</td><td>le: Structural analysis of</td></an5<>	A;Tit]	le: Structural analysis of
Query	19.3%; Score 794.5; D	A; rere A; Acce	srence number: A40136; MUID:90 8881on: A40136
Best I Matche	.9%; Pred. No. 1.9e-41; e 64: Mismatches 268: I	A;Stat	500
		A;Resi	idues: 1-114
ŝ	28 KLOEFVNKKGLLGNRNCCRGGSGPPCACRTFFRVCLKHYQAS 69 : : : : :	A; Acces	38-rerere 38sion: B
QQ	508 KINEFLCOCPKGFSGHLCQYDVDECASTPCKNGAKCLDGPNTYTCVCTEGYTGTHC 563	A;Stat	cus: prelim
ò	70VSPEPPCTYGSAVTPVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPG 117	A; Resi	dues: 181-2
Ωρ		A;Acce A;Stat	sesion: (:us: pre]
Š	118 TESLIIEALHTDSPDDLATENPERLISRLTTORHLTVGEEWSODLHSSGRIDLR 171	A; Mole	ecule type: DNA dues: 'K'.747-821.898-978 <
i i		R, Hure	sh, D.A.; Andrews, M.E.; Raff
Q A	623 NYYLCLCLKGTTGPNCEINLDDCAS-NP	Science A, Titl	se 237, 1487-1490, 1987 le: A sea urchin gene encode
ò	RPR	A;Refe	brence number: A29316; MUID
QQ	660 DGYECACEPGYTGSMCNVNIDECAGSPCHNGGTCEDGIAGFICRCPEGYHDPTCLSE 716	A, Stat	tus: pre
ò	204GDRGEKM-CDPGWKGQYCTDPICLPGCDDQ-HGY 235	A, Mole A, Resi	scule type: mRNA dues: 'S',280-481,786-1064
, de		A, Cros	38-references: GB:M17421; NI
3	VIDEONOINE CERTIFICATION OF THE CENTRAL CONTROL OF THE CONTROL OF	FASEB	J. 3, 1760-1764, 1989
ò	236 CDKPGECKCRVGWQGRYCDECIRYPGCVHGTC	A;Tit] A;Refe	le: Avidin-l erence numbe
Q	776 VCTCREGFSGPNCQTNINECASNPCLNQGTCIDDVAGYKCNCPLPYTGATCEVVL 830	A; Cont	cents: annotation ment: EGF homology repeats
ò	THHKPCRNGA'	F; 1-19)/Domain: signal sequence
Dp	831 APCATSPCKNSGVCKESEDYESFSCVCPTGWQGQTCEIDINECV-KSPCRHGASCQNT-N 888	F; 20-1	1064/Froduct: fibropellin 54/Domain: EGF homology <
ò	309 GSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSCTCPPGFYGKVCELSAMT 368	F;57-1 F;180-	175/Domain: Cir/Cis repeat -211/Domain: EGF homology
;	GSVPCI.COAGSTGRNCESDIIDCRPNPGGSCTDGVNAARCDCI.BGROGAFCREDINE 9	F;218-	-249/Domain: EGF homology
ŝ	s do inclução i i denceso i donceso i por comodoci do vinas como por gone caso ina	F; 294-	.325/Domain: EGF homology

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uEGF gene in the sea urchin Strongylocentrotus purpur
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tus predicted <SIG>
tatus predicted <FIB>
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factor homolog precursor
ibropellin Ib (EGFI)
ratus (purple urchin)
ion 17-Sep-1997 #text_change 09-Jul-2004
; A29316; A43131
D.R.; Hursh, D.A.; Raff, R.A.
                                                           PCANGGTCRDSVNDFSCTCPPGYTGKNCSAPVSRCEHAP
                                                                                                                                          : | | | | | wtgencovlsvscevaaqkrgidvtllcqhgglcvdeed
----YCHCQAGYTGSYCEDEVDECSPNPC-----QNG
                                                                                                                                                                                                                                                               | :|| : :|: : | : | | V---AGYHGSNCSEEINECLSQPCQNGGTCIDLTNTYKC
                                                                                                                                                                                   VLLLLLGCAAVVVCVRLKLQKHQPPPEPCGGETETMNNL
                                                                                                                         - PPPGPMVVDLSE
                                                                                                                                                                                                                                            TNKKADFHGDHGAEKSSFKVRYPTVDYNLVRDLKGD---
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319677; PMID:3498216
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g161474; PIDN:AAA30050.1; PID:g552260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB:X17530; NID:g10225; PID:g667061
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                                                                                                                                                                                                                                                                                                                                   LDPASRSPKC 1238
                                                                                                                         YGGPNCOFLLPE---
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pattern

its

and

gene Notch

PID:94338

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PIDN: CAA48831

19

Gaps

82;

Indels

2437;

Length

98

207

254

302

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---NECSSNPCIHGSCLDQIN-SYRCVCEAGWMGRNCDININECLSNPCVNGG-TCKDMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---TDPICLPG--CDDQHGYCDKPGECKCRVGWQGRYCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSAPVSRCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCRGGSGPPCA----CRTFFRVCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGAG
                                                                                                                                                                                                                                                                                                                                                                                            -RKPCDYGKCIDKINGYECVCEPGYSG
                                                                                                                                                                                                                                                                                                                                                                                                                          --IDPAFSNPIRFPFGFTWPGTFSLIIEALHTDSPDDLATENPERLISRLTTQRHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                       -IDGVNSFTCLCPDGFRDATCLSQH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVGEEWSQD--LHSSGRTDLRYSYRFVCDEHYYGEGCSV---FCRPRDDAFGHFTCGDRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGYLCTCRAGFSGPNCOMNINECASNPCLNQGSCIDDVAGF-----KCNCMLPYTGEVCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -CIRYPGCVHGTCQ-----QPWQCNCQEGWGGLFCNQDLNYCTHHKPCRNGATCTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGOGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSCTCPPGFYGKVCELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCGSSPCSNGAKCVDLGNS
                                                                                                                             ; NID:9433866; PIDN:
mology; EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Motch B protein - mouse (fragment)

N;Alternate names: Notch homolog
C;Species: Mus musculus (house mouse)
C;Date: 21-Jan-1994 #sequence revision 05-Jan-1996 #text_cha
C;Accession: A49175; PH1570; $32113
R;Lardelli, M.; Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A;Title: Motch A and Motch B--two mouse Notch homologues coe
A;Reference number: A49175; MUID:93178563; PMID:8440332
A;Accession: A49175
A;Status: preliminary; nucleic acid sequence not shown
                                      ne of the Drosophila neurogenic MUID:94128602; PMID:8297791
765.5; DB 2;
No. 1.2e-39;
smatches 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1092
                                                                                                                                                                                                                                                                                                 Score 765.5; I
Pred. No. 1.2e
7; Mismatches
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                                                                                                                                                                                                                                                                                                ch 18:6%;
1 Similarity 32.9%;
168; Conservative
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Best Local (
Matches 16)
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77,484-495/Disulfide bonds: #status predicted
5,522-533,527-542,544-553,560-571,565-580,582-591
37,831-846,848-857,864-875,869-884,886-895,902-91
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188;
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Pred. No. 2.5e-4
; Mismatches 1
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S42612
transmembrane protein precursor - zebra f
C;Species: Brachydanio rerio (zebra fish)
C;Date: 20-Feb-1995 #sequence_revision 20
C;Accession: S42612
     <EG06>
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  EGF homology
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;370-401/Domain:
;408-439/Domain:
;446-477/Domain:
;446-477/Domain:
;522-553/Domain:
;522-553/Domain:
;598-629/Domain:
;598-629/Domain:
;674-705/Domain:
;712-743/Domain:
;712-7451-466,468-477,
;7451-466,468-477,
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Best Local S
Matches 174
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A; Molecule type: mRNA
A; Residues: 1-1203 <LAR>
A; Residues: 1-1203 <LAR>
A; Residues: 1-1203 <LAR>
A; Residues: 1-1203 <LAR>
A; Cross-references: UNIPROT:035516; EMBL:X68279; NID:g287989; PIDN:CAA48340.1; PID:g2879
A; Experimental source: embryo
A; Note: sequence extracted from NCBI backbone (NCBIP:126158)
C; Comment: This protein has many EGF repeats and lin-12/Notch repeats.
C; Comment: This protein is one of the neurogenic proteins controlling the decision betwe C; Superfamily: Notch protein; ankyrin repeat homology; EGF homology
F; 143-174/Domain: EGF homology <EGX1>
F; 560-591/Domain: EGF homology <EGX2>
F; 674-705/Domain: EGF homology <EGR3>
F; 712-743/Domain: EGF homology <EGR3>
F; 836-867/Domain: EGF homology <EGR3>
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                                                                                                                                                                                                                                                       Length 1203;
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Best Local Similarity 32.2%; Pred. No. 1.2e-39;
Matches 186; Conservative 61; Mismatches 216;
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GenCore version 5.1.6
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model 38 using protein search, OM protein

Seconds 2004, 13:12:09 29, November Run on:

updates/sec ; Search time 86.9238 (without alignments) 4779.132 Million cell t

US-09-783-931-12 4121

score: Title: Perfect

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Scoring table:

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1825181 segs, 575374646 residues Searched:

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Database

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ALIGNMENTS

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SEQUENCE FROM N.A.

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STRAIN=C57BL/6; TISSUE=Mouse;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MALSCHUL S.F., Zeeberg B., Buetow K.H., Schaefer C.R., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley W.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Mones S.J., Marra M.A.;

Mones S.J., Marra M.A.;

"Marra 
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to the EMBL/GenBank/DDBJ databases.
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STRAIN=C57BL/6; TISSUE=Mouse;
Strausberg R.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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STRAIN=C57BL/6J;
Nagaraja R., Waeltz P.
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Delta-like 1.
Name=Dll1;
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Brathwaite M., Waeltz P., Dudekula D., Nagaraja R.;
Brathwaite M., Waeltz P., Dudekula D., Nagaraja R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 8 EGF-like domains.
EMBL; BCO65063; AAH65063.1; --
EMBL; BCO65063; AAH65063.1; --
EMBL; AX497019; AAR30869.1; --
EMBL; AX497019; AAR30869.1; --
EMBL; AX497019; AAR30869.1; --
EMBL; AX497019; AR30869.1; --
EMBL; AX497019; AR30869.1; --
EMBL; AX497019; AR30869.1; --
EMBL; AX497019; ARS00650.1; --
EMBL; AX497019; ARS00152; F:Protein binding; IPI.
GO; GO:0007368; P:Cetermination of left/right symmetry; IMP
RO; GO:0007368; P:Cetermination of left/right symmetry; INF
RO; GO:0007368; P:Cetermination; IMP.
RITHERPRO; IPR00174; DSL.
RITHERPRO; IPR00174; EGF_Ca.
RITHERPRO; IPR006209; EGF_TIK.
RITHERPRO; IPR006209; EGF_TIK.
REMM; PF00144; DSL; 1.
REMART; SM0019; EGF10.
REMART; SM0019; EGF10.
REMART; SM0019; EGF10.
REMART; SM0019; EGF10.
REMART; SM0010; EGF10.
REMART; SM0019; EGF2; 8.
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REMART; 
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STRAIN-C57BL/6; TISSUE-Mouse;

STRAIN-C57BL/6; TISSUE-Mouse;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Alakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Alones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human and man and ö 900 600 999 9 720 720 120 9 9 Gaps Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus ö 722 Indels Length SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Mouse;
Strausberg R.;
Strausberg R.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC057400; AAH57400.1; -.
SEQUENCE 722 AA; 78449 MW; 9D570B9DC7EEC75E CRC64; and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2] Created) Last sequence update) Last annotation update) Score 4007; DB 2; Pred. No. 4.6e-269; 3; Mismatches 16;

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; F
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
NCBI_TaxID=10090;
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STRAIN=C57BL/6J;
Brathwaite M., Waeltz P., Dudekula D., Nagaraja R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databa:
EMBL; AY497019; AAR30869.1; -.
SEQUENCE 722 AA; 78449 MW; 9D570B9DC7EEC75E CRC6
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STRAIN=C57BL/6; TISSUE=Mouse;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H
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"Generation and initial analysis of more than 15,000 full-length hu and mouse cDNA sequences.",
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Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases
EMBL; BC065063; AAH65063.1; -.
SEQUENCE 722 AA; 78449 MW; 9D570B9DC7EEC75E CRC64;
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Pred. No. 4.6e-269
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STRAIN=C57BL/6; TISSUE=Mouse
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Proc. Natl. Acad.
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                             720
                                                           720
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

STRAIN=C57BL/6 X BALB/c; TISSUE=Embryo;

MEDLINE=95401858; PubMed=7671806;

MEDLINE=95401858; PubMed=7671806;

A Bettenhausen B., de Angelis M.H., Simon D., Guenet J.-L., Gossler A.;

"Transient and restricted expression during mouse embryogenesis of D11, a murine gene closely related to Drosophila Delta.";

Development 121:2407-2418(1995).

-I- FUNCTION: May be involved in cell-to-cell communication in mammalian embryos. May have a role in cellular interactions

underlying somitogenesis and development of the nervous system.

-I- SUBCELLULAR LOCATION: Type I membrane protein.

-I- SUBCELLULAR LOCATION: Type I membrane protein.

-I- TISSUE SPECIFICITY: In the embryo, expressed in the paraxial mesoderm and nervous system. Expressed at high levels in adult heart and at lower levels, in adult lung.

-I- DEVELOPMENTAL STAGE: Expressed until day 15 in the embryo.

Expression then decreases and increases again in the adult.

-I- SIMILARITY: Contains 1 DSL domains.
                           RDTKCQSQSLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVIAT
601 DVSVSIIGATQIKNTNKKADFHGDHGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHSK
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7; C:integral to plasma membrane; ISS.
2; F:Notch binding; IPI.
5; F:protein binding; IPI.
6; P:cell fate determination; ISS.
6; P:compartment specification; IMP.
7; P:embryonic development (sensu Mammalia); NAS.
7; P:hair cell fate commitment; NAS.
7; P:hemopoiesis; ISS.
7; P:neurogenesis; NAS.
9; P:notch signaling pathway; ISS.
9; P:notch signaling pathway; ISS.
5; P:regulation of cell adhesion; ISS.
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                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Delta-like protein 1 precursor (Drosophila Delta homolog
                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; E
Sciurognathi; Muridae;
                                                                                                                                                                                                722 AA
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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I48324.
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G0:0005576; C
G0:0005887; C
G0:0005112; F
G0:0007386; P
G0:0007386; P
G0:0007386; P
G0:0007389; P
G0:0007399; P
G0:0007399; P
G0:0007399; P
G0:0007399; P
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I48324; I
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       HYYGEGCSVFCRPRDDAFGHFTCGDRGEKMCDPGWKGQYCTDPICLPGCDDQHGYCDKPG
                                                          RDTKCQSQSLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVIAT
                                                                                                                                                                                               VSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDLSERHMESQG
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Sciurognathi; Muridae; Murinae; Rattus
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Disiblo G., Hebshi L., Boulter J., Weinmaster G.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: May be involved in cell-to-cell communication in mammalian embryos. May have a role in cellular interactions underlying somitogenesis and development of the nervous system similarity).

-!- SUBUNIT: Interacts with Notch receptors.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- SIMILARITY: Contains 1 DSL domain.
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P97677;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Delta-like protein 1 precursor (Drosophila Delta hom Name=Dll1;
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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Potential.

Extracellular (Potential Potential).

Cytoplasmic (Potential).

DSL.

EGF-like 1.

EGF-like 3.

EGF-like 4, calcium-bind EGF-like 6.

EGF-like 6.

EGF-like 7, calcium-bind EGF-like 8.

EGF-like 8.

EGF-like 9.

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EGF-like 4, calcium-bind EGF-like 8.

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EGF-l
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1.8e-269;
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Pred. No. 8.8e-
4; Mismatches
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  Asx_hydroxyl_DSL.
EGF_2.
EGF_Ca.
EGF_II.
EGF_II.
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InterPro; IPR000152; Asx_hydrox; InterPro; IPR00174; DSL.
InterPro; IPR00143; EGF_2.
InterPro; IPR001438; EGF_II.
InterPro; IPR00163; EGF_II.
IPR0SITE; PS00102; EGF_II
                                                                                                                                      ; EGFBLOOD.
0; ASX HYDROXYL;
2; EGF_1; 8.
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6; EGF_3; 7.
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000548; Q9NU41; Q9UJV2;

15-JUL-1998 (Rel. 36, Created)

15-JUL-1998 (Rel. 44, Last annotation update)

05-JUL-2004 (Rel. 44, Last annotation update)

Delta-like protein 1 precursor (Drosophila Delta hor (H-Delta-1) (UNQ146/PR0172).

Name=DLL1;

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae

NCBI_TaxID=9606;
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les 28;
4B8EE2272BAEA27E
               Score 3848; D. Pred. No. 4.7e
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=21464863; PubMed=11581320;
Maleco A.C., Neves H., Hooijberg E., Gameiro P., Clode N., Haury M Jaleco A.C., Neves H., Hooijberg E., Gameiro P., Clode N., Haury M Henrique D., Parreira L.;

"Differential effects of Notch ligands Delta-1 and Jagged-1 in hum lymphoid differentiation.";

J. Exp. Med. 194:991-1001(2001).

-I- FUNCTION: Acts as a ligand for Notch receptors. Blocks the differentiation of progenitor cells into the B-cell lineage wh promoting the emergence of a population of cells with the characteristics of a T-cell/NK-cell precursor.

-I- SUBCBLLULAR LOCATION: Type I membrane protein.

-I- SUBCBLLULAR LOCATION: Type I membrane protein.

-I- TISSUE SPECIFICITY: Expressed in heart and pancreas, with lowe expression in brain and muscle and almost no expression in placenta, lung, liver, and kidney.

-I- SIMILARITY: Contains 1 DSL domains.

-I- SIMILARITY: Contains 8 EGF-like domains.
               SEQUENCE FROM N.A.
MEDLINE=99180765; PubMed=10079256;
Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,
Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas
"Human ligands of the Notch receptor.";
Am. J. Pathol. 154:785-794(1999).
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Han W., Ye Q., Moore M.A.S.;
"A soluble form of human delta-like-1 inhibits differentiation hematopoietic progenitor cells.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dc Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansun Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W. Godowski P.;
"The secreted protein discovery initiative (SPDI), a large-scalefort to identify novel human secreted and transmembrane proteinformatics assessment.";
Genome Res. 13:2265-2270(2003).
                                                                                                                                                                                                                                                     [3]
SEQUENCE FROM N.A.
Oda T., Chandrasekharappa S.C.;
"Human Delta 1 gene sequence.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
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EMBL; AF196571; AAF05834.1; -
EMBL; AF222310; AAG09716.1; -
EMBL; AY358892; AAQ89251.1; -
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EMBL; AL078605; CAB895
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Pred. No. 8.3e-225,
73; Mismatches 72,
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SEQUENCE FROM N.A.

TISSUE=Spinal cord;
MEDLINE=95319507; PubMed=7596411;
Henrique D., Adam J., Myat A., Chitnis A "Expression of a Delta homologue in proschick.";
Nature 375:787-790(1995).
EMBL; U26590; AAC59689.1; -.
FIRE 150719; 150719.
HSSP; P00740; 1EDM.
GO; GO:0016020; C:membrane; IEA.
GO; GO:001520; F:calcium ion binding; I GO; GO:0007154; F:calcium ion binding; I InterPro; IPR000152; Asx hydroxyl_S.
InterPro; IPR00152; Asx hydroxyl_S.
InterPro; IPR00143; EGF_C.
InterPro; IPR00143; EGF_I.
InterPro; IPR001438; EGF_II.
InterPro; IPR0010138; EGF_II.
InterPro; IPR001019; EGF_II.
Ffam; PF01414; DSL; 1.
Ffam; PF00110; ASX HYDROXYL; 3.
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01-NOV-1996 (TrEMBLrel. 01, Last
01-MAR-2004 (TrEMBLrel. 26, Last
C-Delta-1.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Cra
Archosauria; Aves; Neognathae; Gallus.
NCBI_TaxID=9031;
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Nakamura K., Kikuchi Y., Susaki K., Chiba C., Submitted (OCT-2002) to the EMBL/GenBank/DDBJ-1- SIMILARITY: Contains 8 EGF-like domains.
EMBL; AB095017; BAC41350.2; -.
HSSP; P00740; 1EDM.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
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Q8AW87;
01-MAR-2003 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
1.1gand Delta-1.
Name=Delta-1;
Cynops pyrrhogaster (Jap Eukaryota; Metazoa; Chor Amphibia; Batrachia; Cau NCBI_TaxID=8330;
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MEDLINE=95319503; Pubmed=7596407;

MEDLINE=95319503; Pubmed=7596407;

Chitnis A., Henrique D., Lewis J., Ish-Horowicz D., Kintner C.;

Chitnis A., Henrique D., Lewis J., Ish-Horowicz D., Kintner C.;

Chitnis A., Henrique D., Lewis J., Ish-Horowicz D., Kintner C.;

Chitnis A., Henrique D., Lewis J., Ish-Horowicz D., Kintner C.;

The Drosophila neurogenic gene Delta.";

Nature 375:761-766(1995).

EMBL; L42229; AAC38017.1; -.

R GO; GO:0016020; C:membrane; IEA.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0005154; P:cell communication; IEA.

InterPro; IPR00142; EGF_Ca.

InterPro; IPR001438; EGF_Ca.

InterPro; IPR001438; EGF_II.

InterPro; IPR006209; EGF_II.

R Pfam; PF01414; DSL; 1.

R Pfam; PF00101; EGFBLOOD.

R PRINTS; PR00010; EGFBLOOD.
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MEDLINE=95319507; PubMed=7596411;
Henrique D., Adam J., Myat A., Chitnis A., Lewis J., Ish-Horowi
"Expression of a Delta homologue in prospective neurons in the
TEKYTEGQNSQFPWIAVCAGIILVLMLLLGCAAIVVCVRLKVQKRHHQPEACR
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3; Mismatches 87;
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SMART; SM00051; DSL; 1.
SMART; SM00179; EGF CA; 4.
PROSITE; PS00010; ASX HYDROXYL; 3
PROSITE; PS01186; EGF 1; 8.
PROSITE; PS01186; EGF 2; 8.
PROSITE; PS01187; EGF 2; 6.
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Nature 375:787-790(1995)
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Pred. No. 1.9e-209;
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GO; GO:0007154; P:cell communication; InterPro; IPR000152; ABX_hydroxyl_S. InterPro; IPR001774; DSL. InterPro; IPR001774; DSL. InterPro; IPR00142; EGF_Z. InterPro; IPR001438; EGF_II. InterPro; IPR006209; EGF_II. InterPro; IPR006209; EGF_II. Pfam; PF01414; DSL; 1. Pfam; PF00008; EGF; 6. PRINTS; PR00010; EGFBLOOD. SMART; SM00179; EGF CA; 6. SMART; SM00179; EGF_Z; 7. PROSITE; PS00100; ASX HYDROXYL; 3. PROSITE; PS01186; EGF_Z; 7. PROSITE; PS01186; EGF_Z; 7. PROSITE; PS01187; EGF_Z; 7. PROSITE; PS01187; EGF_Z; 2. EGF_Iike domain.
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MEDLINE=22248969; PubMed=12361969;
Hans S., Campos-Ortega J.A.;
"On the organisation of the regulatory region of the zebrafish deltaD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Q8UWJ4
Q8UWJ4;
Q8UWJ4;
Q8UWJ4;
Q8UWJ4;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DeltaD protein.
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID=7955;
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Pred. No. 2.6e-187;
98; Mismatches 120;
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Bevelopment 129:4773-4784 (2002).

EMBL; AF426384; AAL31528.1; -.

HSSP; P00740; 1EDM.

GO; GO:0016020; C:membrane; 1EA.

GO; GO:0005509; F:calcium ion binding; IJ

GO; GO:0007154; P:cell communication; 1EI

GO; GO:0007154; P:cell communication; 1EI

InterPro; IPR00152; Asx_hydroxyl_S.

InterPro; IPR00152; Asx_hydroxyl_S.

InterPro; IPR00152; EGF_Ca.

InterPro; IPR00142; EGF_Ca.

InterPro; IPR001438; EGF_II.

InterPro; IPR001631; EGF_Ca.

InterPro; IPR001631; EGF_Ca.

InterPro; IPR001019; EGF_II.

Pfam; PF01414; DSL; 1.

Pfam; PF01114; DSL; 1.

PFAMRT; SM0010; EGFELOOD.

SMART; SM001019; EGF_CA; 4.

PROSITE; PS001186; EGF_Z; 8.

PROSITE; PS01187; EGF_Z; 8.

PROSITE; PS01187; EGF_CA; 2.

EGF-like domain.
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e-187;
                                                                                                             Score 2823.5;
Pred. No. 4.1e
8; Mismatches
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Potential.
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PS00010; ASX HYDROXYL;
PS00022; EGF_1; 8.
PS01186; EGF_2; 8.
PS50026; EGF_3; 6.
PS01187; EGF_CA; 2.
domain; Signal; Transme
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79061 MW;
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milarity 66.3%;
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01-OCT-2004
01-OCT-2004
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Best Local Sim:
Matches 487;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
EGF-like
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XXQSVFV
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P87357;

O1-MAY-1997 (TrEMBLrel. 03, Created)

O1-MAY-1997 (TrEMBLrel. 03, Last sequence update)

O1-MAY-1997 (TrEMBLrel. 26, Last annotation update)

F 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DeltaD transmembrane protein precursor.

Name=dld; Synonyms=deltaD;

Brachydanio rerio (Zebrafish) (Danio rerio).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

Cyprinidae; Danio.

NCBI_TaxID=7955;
            neuroge
                                                           SEQUENCE FROM N.A.

KEDLINE=97346722; PubMed=9203139;

MEDLINE=97346722; PubMed=9203139;

Dornseifer P., Takke C., Campos-Ortega J.A.;

Dornseifer P., Takke C., Campos-Ortega J.A.;

Dornseifer P., Takke C., Campos-Ortega J.A.;

BOUNGERSION Of a zebrafish homologue of the Drosophila neu:

Gevelopment.";

Mech. Dev. 63:159-171(1997).

Rembl; Y11760; CAA72425.1; -.

Replace Conference of the Drosophila neu:

Replace Conference of the Drosophila neu:

Replace Conference of the Drosophila neu:

Replace Conference of PR001438; EGF_CA:

Replace Conference Communication; IEA.

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Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
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             (Danio rerio).
; Craniata; Vertebrata; Euteleostomi;
Teleostei; Ostariophysi; Cypriniformes
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TISSUE=Embryo;

Strausberg R.;

Strausberg R.;

Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
EMBL; BC075742; AAH75742.1; -.

Hypothetical protein.

SEQUENCE 772 AA; 84968 MW; 716A014158938576 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.4%; Score 2778; DB 2; 62.3%; Pred. No. 6.3e-184; ive 87; Mismatches 131;
                                                                                 SEQUENCE FROM N.A.
TISSUE=Embryo;
MEDLINE=22388257; PubMed=12477932
Hypothetical protein.
Brachydanio rerio (Zebrafish) (
Eukaryota; Metazoa; Chordata; C
Actinopterygii; Neopterygii; Te
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity 62.3
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C 057462;
C 057462;
T 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
T 01-JUN-1998 (TrEMBLrel. 26, Last annotation update)
T 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
E DeltaA.
Name=dla, Synonyms=deltaA;
Name=dla, Synonyms=deltaA;
S Brachydanio rerio (Zebrafish) (Danio rerio).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
C Cyprinidae; Danio.
X NCBI TaxID=7955;
N [1]
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                                 CSAPVSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDLSERHM
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Appel B., Eisen J.S.;
"Regulation of neuronal specification in belta function.";
Development 125:371-380(1998).
EMBL; AF030031; AAC41249.1; -.
HSSP; P00740; 1EDM.
ZFIN; ZDB-GENE-980526-29; dla.
GO; GO:0005509; F:calcium ion binding; IS
GO; GO:0005509; F:calcium ion binding; IS
InterPro; IPR00152; Asx hydroxyl_S.
InterPro; IPR00152; Asx hydroxyl_S.
InterPro; IPR00142; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR001438; EGF_II.
InterPro; IPR0016209; EGF_II.
InterPro; IPR0016209; EGF_II.
SMART; SM00051; DSL; 1.
SMART; SM00051; DSL; 1.
SMART; SM00051; DSL; 1.
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PROSITE; PS00022; EGF_1; 8.
PROSITE; PS01186; EGF_2; 8.
PROSITE; PS50026; EGF_3; 6.
PROSITE; PS01187; EGF_CA; 1.
EGF-like domain.
SEQUENCE 802 AA: RROAT PT.
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                                                                  Euteleost; Pipidae;
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Q7ZXT4;
Q7ZXT4;
Q1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
MGC52561 protein.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pip Xenopodinae; Xenopus.
NCBI_TaxID=8355;
[1]
SEQUENCE FROM N.A.
TISSUE=Embryo;
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Score 2713; DB 2
Pred. No. 2.1e-17
93; Mismatches 13
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ch 65.8%; l Similarity 62.6%; 473; Conservative 5
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Richards R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Galbas R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human and initial analysis of more than 15,000 full-length human
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"Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative.";
Dev. Dyn. 225:384-391(2002).
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TISSUE=Embryo;
MEDLINE=22341132; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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48.1%; Pred. No. 2.3e-123;
ive 100; Mismatches 184;
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TISSUE=Embryo;
Klein S., Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank,
EMBL; BC044262; AAH44262.1; -.
HSSP; P00740; 1EDM.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005509; F:calcium ion binding; I]
GO; GO:0007154; P:cell communication; IEI
InterPro; IPR00152; ABx_hydroxyl_S.
InterPro; IPR001774; DSL.
InterPro; IPR00143; EGF_Ca.
InterPro; IPR00143; EGF_TI.
InterPro; IPR00143; EGF_TI.
InterPro; IPR00143; EGF_TI.
InterPro; IPR00143; EGF_TI.
InterPro; IPR006209; EGF_TI.
InterPro; IPR00645; EGF_TI.
PubMed=12477932
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PRINTS; PR00010; EGFBLOOD.
SMART; SM00051; DSL; 1.
SMART; SM00179; EGF CA; 3.
PROSITE; PS00010; ASX HYDROXYL; 2
PROSITE; PS01186; EGF 1; 8.
PROSITE; PS01186; EGF 2; 7.
PROSITE; PS01187; EGF 2; 7.
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MEDLINE=22388257;
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Kuz; Notch; differentiation; cervical; breast; colon; cancer; melanoma; seminoma; central nervous system disorder; psoriasis regeneration; liver cirrhosis; keloid formation; baldness; ear disorder; chick. lung; m tissue

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(UYYA) UNIV YALE

Ħ ö Rand MD, ŝ Artavanis-Tsakonas

WPI; 2000-282852/24.

for diagnosis, nervous system, and antibodies useful disorders of central a New cleavage peptide, nucleic acids prevention and treatment of cancer, cirrhosis and psoriasis.

3; 177pp; English Claim 1; Fig

Units sequence represents the chack accelin anno acid sequence.

Delta is a toporythmic protein that contains a sequence which is cleaved by the metalloprotease-disintigrin Kuzbanian (Kuz). Cleavage by Kuz results in two fragments a soluble amino terminal fragment consisting casantially of the extracellular domain, and a membrane bound fragment consisting of the transmembrane domain, and a membrane bound fragment of differentially of the transmembrane domain and the intracellular domain. The soluble fragment is abbt to bind to Notch. Delta plays a key role in differentiation, and therefore detection and measurement of delta activation is important in the study of differentiation. The invention relates to the delta cleavage peptides (the activation. Delta cleavage peptides and chimeric proteins are useful for modulating the activity of methods for detecting and measuring delta activation. Delta cleavage peptides, and chimeric proteins are useful for modulating the activity of or organism, expressing Norch. We contacting a cell with kuz protein or nucleic acid or its antibody, the activity or levels of delta protein is or organism, expressing the artivity or levels of delta protein is modulated and vice versa. A delta cleavage peptide or its derivative capable of binding kuz protein is useful for treating or preventing a disease or disorder associated with increased delta activity or expression such as cervical, breast, colon or lung cancer, melanoma or seminoma in humans. A recombinant cell comprising a delta protein binding activity or protein and kuz is useful for the diagnosis of disease or clasventing the ability of delta cleavage peptide is useful for the diagnosis of disease or disorder associated with increased levels of or predisposition to developing a disease or disorder associated with aberrant levels of the complex, comprising measuring the ability of delta cleavage peptide is useful for the diagnosis of disease or disorder associated with aberrant levels of complex, complex, comprising delta or prom delta protein amino acid sequence. : contains a sequence which is cleaved This sequence represents the chick

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RCEH-PCHNGATCHRR----YCECA-GYGG-NCQFLLPEPP-GPV.

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KOKPEC - - ETETMNNLANCOREKD - -

FPW-AVCAGLVL

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728 AA; Sequence

144; Length 728; Indela 13; Score 2483; DB 3; Pred. No. 5.6e-113 ; Mismatches 20 9 13.4%; ilarity 75.9%; Conservative Similarity 545; Conser Query Match Best Local S Matches 545

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This sequence represents the murine delta protein amino acid sequence. Delta is a toporythmic protein that contains a sequence which is cleaved by the meteralloprotease-dishintigrin (Kuzbanian (Kuz). Cleavage by Kuz results in two fragments, a soluble amino terminal fragment consisting essentially of the extracellular domain, and a membrane bound fragment consisting creatist transmembrane domain and the intreacellular domain. The consisting of the transmembrane domain and the intreacellular domain. The soluble fragment is able to bind to Notch. Delta plays a key role in differentiation, and therefore detection and measurement of delta activation is important in the study of differentiation. The invention relates to the delta cleavage peptides (the active fragment), and to methods for detecting and measuring delta activation. Delta cleavage peptides, and chimmeric proceins are useful for modularing the activity of notch, delta or kuz or at least one of the signalling pathways in a cell notch, delta or kuz or at least one of the signalling pathways in a cell conclet cand or its antibody, the activity or levels of delta protein is modulated and vice versa. A delta cleavage peptide or its derivative modulated and vice versa. A delta cleavage peptide or its derivative capable of binding kuz protein is useful for treating or preventing a disease or disorder associated with increased delta activity or expension such as cervical, breast, colon or lung cancer, melanoma or seminoma in humans. A recombinant cell comprising a delta peptide is useful for the diagnosis of diseases or disorders associated with increased levels of delta cleavage peptide is useful for the diagnosis of delta cleavage peptide is useful for the diagnosis of delta cleavage peptide is useful for the diagnosis of delta cleavage peptide is useful for the presence of, or predisposition to complex, comprising measuring the ability of delta cleavage peptide is useful for the presence of, or predisposition to complex, comprising measuring the period of th
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tissue regeneration; Notch; cervix cancer; breast cancer;
colon cancer; melanoma; seminoma; neurogenesis; therapy.
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have also been identified. Delta-1 proteins can be used to treat or prevent disorders characterised by increased Notch activity, such as cervical, breast, lung or colon cancer, melanoma or seminoma, as well nervous system disorders, and to promote tissue regeneration and repai
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17-APR-2001;
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The invention relates to modulating the differentiation of an embryonic stem cells, comprising; (a) providing a culture of embryonic stem cells, (b) providing at least one ligand or its active binding fragment, capable of binding its coprate receptor polypeptide expressed by the embryonic stem cells and the ligand; and (d) growing a culture comprising embryonic stem cells and the ligand call fransfered with a nucleic acid molecule selected from: of embryonic stem cells, (i) forming a culture comprising embryonic stem cells and the providing a cell fransfered with a nucleic acid molecule selected from: of embryonic stem cells, (ii) any office of the mucleic acid molecule selected from: of embryonic stem cells and the dight seek to the mucleic acid selected from: of capable of modulating embryonic stem cell dight capable of binding a writ receptor; or (iii) nucleic acid molecules which are degenerate as a result of the genetic code to the abunceance and/or differentiation of the embryonic stem cells, or (ii), by forming a culture comprising the cell identified in (a) with an embryonic stem cells, (b) forming a culture for the maintenance and/or differentiation of the embryonic stem cell; (a) Inhibiting the differentiation of embryonic stem cell; and (c) growing the cell identified in (a) with an embryonic stem cell; and (c) growing the cell; dentified in (a) much an embryonic stem cell; and (c) drowing the cell; dentified in (a) much an embryonic stem cell; and (c) drowing the cell; dentified in (a) much and cells and molecule selected from; (i) a molecule become a polypeptide or itse active comprising the cell; and molecule selected from; (i) a molecule by onlypeptide capable of inhibiting which signalling.

C (i) and encodes a polypeptide capable of inhibiting with an embryonic stem cell; and (ii) and encodes a polypeptide capable of inhibiting with an embryonic stem cell; dentified in (a) with an embryonic stem cell; dentified or (d) growing the cellidentified in (a) with an embryonic stem cell; dentified or (
Notch; Wnt; embryonic stem cell; embryogenesis; human; differentiation; ligand; Parkinson's disease; Huntington's disease; motor neuron disease; heart disease; diabetes; liver disease; cirrhosis; renal disease; AIDS; acquired immunodeficiency syndrome.
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t disease,
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the identification of biologically active agents which mediate their
effect through the activation of genes. The method involves providing a
copulation of cells stably transfected with a nucleic acid encoding a
reporter molecule, cloning the transfected cells into a cell array,
coposing the array to at least one agent to be tested and detecting a
signal generated by the reporter molecule as a result of exposure to the
agent. The method is useful in identifying biologically active agents and
the genes through which the agents act, in screening potential drugs for
their ability to activate certain drug targets in a high-throughput
assay, in identifying relationships between signalling pathways and
specific signals that could be useful in eventually directing the
differentiation of embryonic stem cells and in toxicology assays by
testing for unwanted activation or inhibition of specific signalling
pathways. The present sequence is murine notch ligand delta-like I
protein used to illustrate the method of the invention
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458 420 540 720 503 Proliferation; differentiation; suppression; human; delta-1; serrate-1; blood cell; neuron; leukaemia; malignant tumour; immunosuppression. The present sequence represents a polypeptide which suppresses proliferation and differentiation of undifferentiated cells such as neurons and blood cells. The polypeptide may be used for the prevention and control of disorders involving undifferentiated cells, such as cella --FPW-AVCAGLV---LLLLGCAA-VVCVRLK-QK----PE-C--ETETMNNLANCQREK --VHKK --EEO-Peptide(s) encoded by human genes delta-1 and serrate-1 - suppress proliferation and differentiation of undifferentiated human blood VSRCEH-PCHNGATCHRR----YCECA-GYGG-NCQFLLPE-PPGP--VD----Differentiation_suppression_protein --KVRYP-VDYNLV--LK--Proliferation and differentiation suppression polypeptide

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                                                                                                                                                                                                This sequence represents the human delta-1 protein, which is a ligand the human notch protein. The protein or fragments, especially AAW75493. W75495, can be used as a drug to control vascular cells. The sequences were isolated and the truncated fragments were generated using the primers AAX16818-X16831
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Pred. No. 5e-109;
11; Mismatches 27
                                                                                                                                                                 comprises
                                        delta-1
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Location/Qualifiers
1. .21
/note= "signal peptic
22. .723
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/note= "mature
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Best Local Similarity 75.1%;
Matches 534; Conservative 1
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N-PSDB; AAX16817.
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                     SALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGGAGPPPCACRTFFRVCLKHYQASVS
                                                                                                   RPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCD-QHG-CDKPGECKCRVGWQGR
                                                                                                                                         GATCHRR----YCECA-GYGG-NCQFLLPE-PPGP--VD----EEQ---FPW-AVCAGL
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1. .21
/label= Signal_peptide
2. .8
/note= "N-myristoylation s
37. .43
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/note= "N-myristoylation 8
40. .46
/note= "N-myristoylation 8
93. .97
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inhibits the
or muscle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lay be used for tumours. They e.g. for he present present
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human
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                                              KNTNKKADFHGDHSADKNGFKARYPAVDYNLVQDLKGDDTAVRDAHSKRDTKCQPQGSSG
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                                                                                                                                                                                                                        differentiation inhibitor; proliferation;
                                                                      578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes full length and shortened human proteins. Human delta-2 is a differentiation inhibitor which in differentiation of undifferentiated cells (other than brain or cells), such as blood cells, and enhances the proliferation of undifferentiated blood cells. Products of human delta-2 may be the treatment of diseases such as leukaemia and malignant tumou may also be used in the culture of human cells in vitro, e.g. f production of supplies of undifferentiated blood cells. The pre sequence represents human delta-1, from an example of the prese
differentiation of undifferentiated bloc
s and other disorders and the culture of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               723;
                                - LKVHKKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139;
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                                                                                 ||
EKGTPTTLRGGEASERKRPDSGCSTSKDTKYQSVYVISEEKDECVIATEV
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Pred. No. 5e-109;
1; Mismatches 27;
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                               --DK---KVRYP-VDYNLV
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75.1%;
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/label=
22. .723
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for treatment of cancer
cells in vitro.
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                               KNTNKK-DFH---
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eukaemia; malignant
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Best Local Similarity
Matches 534; Conser
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391. .403

/label= EGF-like_domain

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/note= "Asr
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152. .261
'note= "Tyrosine kinage
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28. .334
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                                                                                                                                                                                                                                                                                                                                                                                             Composition for inhibiting neoplastic cell growth and treating cancers ovary, uterus, prostate, lung and bladder, comprises PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptide or their agonist.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Compositions comprising a PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptide or their agonists, mixed with a carrier is useful for inhibiting neoplastic growth and treating tumors such as cancers of breast, ovary, renal, colorectal, uterus, prostate, lung, bladder, central nervous system, melanoma and leukaemia
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          membrane lipoprotein lipid
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/note= "N-myristoylation site"
698. .702
/note= "Casein kinase II -hoor"
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75.1%; Pred. No. 5e-109
ive 11; Mismatches
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/note= "Casein kinase II
676. .682
/note= "N-myristoylation
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                                                                       phosphorylation site"
670. .674
/note= "Casein kinase 1
671. .675
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552. .563
/label= Prokaryotic
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/note= "cb/
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N-PSDB; AAZ93703.
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                                     SAMTCAD
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 NTGOGSY
                                                                  GPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDLGNSY-C-CQ
                                                                                                                                                              --EEQ---FPW-AVCAGL
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                      TCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYGK-CEL
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YCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCKNGATCT
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99US-0123618P.
99US-0123957P.
99US-0125775P.
99US-0128849P.
99WO-US008615.
99US-0131445P.
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12-MAR-1999;
23-MAR-1999;
12-APR-1999;
20-APR-1999;
28-APR-1999;
14-MAY-1999;
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The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases of the central and clisease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases, allergic diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases, allergic diseases, inflammatory and transplantation associated diseases including graft rejection and graft-versus-host-disease. AAC58397 to AAC58378 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAC58642 and AAB33414 to AAB33477 represent human PRO polynucleotide and protein sequences given in the cremplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              es, useful in the diagnosis and treatment of e.g. systemic lupus erythematosis, rheumatoid thyroiditis and diabetes mellitus.
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DL, Smith
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Yan M;
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D, Shelton
Wood WI, Ya
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an J, Pennica
Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309pp; English
99WO-US012252.
99US-0144758P.
99US-0144758P.
99US-0146222P.
99WO-US020111.
99WO-US020111.
99WO-US021547.
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99WO-US028313.
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99WO-US028551.
99WO-US028551.
99WO-US028563.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sixty four PRO polypeptides, immune related disorders, e.g arthritis, osteoarthritis, the
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Tumas D,
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N-PSDB; AAC58587.
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02-JUN-1999;
23-JUN-1999;
26-JUL-1999;
26-JUL-1999;
01-SEP-1999;
03-SEP-1999;
13-SEP-1999;
15-SEP-1999;
15-SEP-1999;
15-SEP-1999;
15-SEP-1999;
15-SEP-1999;
05-OCT-1999;
01-DEC-1999;
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02-DEC-1999;
06-JAN-2000;
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11-FEB-2000;
18-FEB-2000;
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Stewart T
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139;

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Score 2401.5; Pred. No. 5e-1 1; Mismatches

Query Match Best Local Similarity 75.1%; Matches 534; Conservative

723 AA;

Sequence

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Length 723;

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The present invention describes nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorder in mammals by modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB24338 to AAB24435 represent nucleotide and protein sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                              useful for preventing, diagnosing r, endothelial or angiogenic
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Best Local Similarity 75.1%; Pred. No. 5e-109;
Matches 534; Conservative 11; Mismatches 27;
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Wood WI;
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, Gurney AL,
Williams PM,
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99US-0115554P.
99WO-US005028.
99US-0123957P.
99US-0131445P.
99WO-US012252.
99US-0141037P.
99US-0144758P.
99WO-US020594.
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N-PSDB; AAA77512.
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12-JAN-1999;
08-MAR-1999;
12-MAR-1999;
28-APR-1999;
02-JUN-1999;
23-JUN-1999;
26-JUL-1999;
01-SEP-1999;
01-SEP-1999;
13-SEP-1999;
15-SEP-1999;
15-SEP-1999;
15-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                           Delta; Kuz; Notch; differentiation; cervical; breast; colon; cancer; lung; melanoma; seminoma; central nervous system disorder; psoriasis, tissue regeneration; liver cirrhosis; keloid formation; baldness; inner ear disorder; human.
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                                         GPCFNGGRC-DNPDGGY-C-CPLG-SGFNCFKK---DCSSPC-NGA-CVDLGN
                                                                                GATCHERGHRYVCECARGYGGPNCQFLLPELPPGPAVVDLTEKLEGGGGPFPW
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EEKGTPTTLRGGEASERKRPDSGCSTSKDTKYQSVYVISEEKDECVIATEV
                                                                                                                                                                                                                                                    -RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IATEV
                                                                                                                                                                 ---LLLGCAA-VVCVRL---KQKPEC----ETETMNNLANCQREKD-
                                                                                                                         GATCHRR----YCECA-GYGG-NCQFLLPE-PPGP--VD--
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consisting of the transmembrane domain and the intracellular domain. The soluble fragment is able to bind to Notch. Delta plays a key role in differentiation, and therefore detection and measurement of delta activation is important in the study of differentiation. The invention relates to the delta cleavage peptides (the activation. Delta cleavage peptides, and chimeric proteins are useful for modulating the activity of peptides, and chimeric proteins are useful for modulating the activity of peptides, and chimeric proteins are useful for modulating the activity of norch, delta or kuz or at least one of the signalling pathways in a cell or or organism, expressing Notch. By contacting a cell with kuz protein or nucleic acid or its antibody, the activity or levels of delta protein is andulated and vice versa. A delta eleavage peptide or its derivative capable of binding kuz protein is useful for treating or preventing useful for treating or preventing central nervous system disorders. A delta cleavage peptide is useful for the diagnosis of diseases or disorder associated with increased levels of Notch-delta protein binding useful for treating or preventing central nervous system disorders. A disorders associated with increased levels of Notch-delta protein binding activity comprising measuring the ability of delta cleavage peptides in a sample to bind kuz protein. A complex of delta protein and kuz is useful for developing a disease or disorder associated with aberrant levels of the complex, comprising measuring the level or functional activity of the complex, comprising measuring the level or functional activity of the complex, comprising measuring the level or functional activity of the complex, comprising measuring the level or functional activity of the complex, comprising each or war in a sample to be peptide is also useful for promoting tissue regeneration and repair, for treating liver cirrhosis, keloid formation, psoriasis, baldness and degenerative or traumatic disorders of the sensory peptide land activ
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/note= "Casein
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leukemia and neoplastic for nsefnl PRO538, PRO172 and PRO182 polypeptides use including cancers of the breast and lung, compounds capable of inhibiting growth of rkU211, PRO228, I treating tumors i for identifying c

Claim 31; Fig 8; 133pp; English.

Isolated PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptides or their agonists (preferably anti-PRO agonist antibody or a small molecule mimicking the biological activity of PRO polypeptide) are useful in vitro or in vivo for inhibiting the growth of a tumour cell. Compositions comprising the PRO polypeptides are useful for inhibiting neoplastic cell growth and for treating cancer including breast, ovarian, renal, colorectal, uterine, prostate, lung, bladder, central nervous system cancer, melanoma and leukaemia in a mammal. The PRO polypeptides are also useful for treating other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal, blastocoelic disorders and inflammatory, angiogenic and immunologic disorders as well as being useful for identifying agonists to PRO polypeptides by contacting the polypeptide with a candidate molecule and monitoring biological activity mediated by the polypeptide

¥ 723 Sequence

67 Gaps 139; Length Indele Score 2401.5; DB 3; Pred. No. 5e-109; 1; Mismatches 27; Query Match Best Local Similarity 75.1%; Pr Matches 534; Conservative 11;

1SY-C-CQ 376 111 132 167 192 220 252 279 312 327 372 432 425 467 492 56 'NTGQGSY ||||||| 'NTGQGSY RVGWQGR EHAPCHN -GCCTFFRVCLKHYQASVS AGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-PVSRCEH-PCHN -AVCAGL SALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGGAGPPPCACRTFFRVCLKHYQASVS DDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFVCDEHYYGEGCSVFC AYLCRCO VAVCAGV RPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCD-QHG-CDKPGECKC GPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDLGN SALLC---VSGVFELKLQEFVNKKGLL-NRNCCRGG-13 73 5 133 168 193 280 313 328 377 433 112 221 253 373 426 g a 셤 a a a g 유 a D 8 ઠે δ ਨੇ ઠે õ õ ઠે ઠે

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SUMMARIES

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US-08-083-590A-2 US-08-465-500-6 US-08-346-126-6 US-08-346-128-6 US-08-893-828-6 US-08-981-392-6 US-09-908-322-6 US-09-908-322-6 US-09-908-322-43 US-09-214-278-5 US-09-855-722-5 US-09-855-722-5 US-09-855-722-5 US-09-855-722-5 US-09-855-722-5 US-09-855-722-5 US-09-855-722-5 US-09-855-722-5 US-09-855-722-5 US-09-855-722-5 US-09-855-722-5 US-09-855-722-5 US-09-855-722-5 US-09-855-722-5	
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ALIGNMENTS

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RESULT 1
US-08-981-392-13
i Sequence 13, Application US/08981392
j Patent No. 6262025
j Patent No. 6262025
j GENERAL INFORMATION:
j APPLICANT: Henrique, Domingos Manuel Pinto
APPLICANT: Gray, Grace
j APPLICANT: Henrique, Domingos Manuel Pinto
APPLICANT: Henrique, Domingos Manuel Pinto
APPLICANT: Gray, Grace
j TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
NUMBER OF SEQUENCES:
j CORRESPONDENCE ADDRESS:
j ADDRESSEE: Pennie & Edmonds LLP
sTREET: 1155 Avenue of the Americas
CITY: New York
sTATE: NY
country: USA
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Pred. No. 3.3
); Mismatches
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ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,392
FILING DATE: 22-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-038
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 578 amino acids
TYPE: amino acids
TYPE: amino acids
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; MOLECULE TYPE: I
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; Sequence 2, Application US/08981392
; Patent No. 6262025
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; APPLICANT: Henrique, Domingos Manuel Pinto
; APPLICANT: Lewis, Julian Hart
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Gray, Grace
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Best Local Similarity 100.0%; Pred. No. 3.3
Matches 578; Conservative 0; Mismatches
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7326-123
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       NAME: Misrock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 732
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                      8
                                                                                         LENGTH: 578 amino acids

TYPE: amino acid

TYPE: amino acid

STRANDEDNESS: <Unknown

TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NC

US-09-908-322-13
ATTORNEY/AGENT
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                                       LISRLTQRHLVGEEWSQDLHSSGRTDLYSYRFVCDEHYYGEGCSVFCRPRDDFGHFTCGR
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i Sequence 13, Application US/09908322

i Sequence, Domingos Manuel Pinto Lewis, Julian Hart Artavanis-Tsakonas, Spyridon Gray, Grace

ITTLE OF INVENTION: NUCLEOTIDE AND PROTEIN USA

ITTLE OF INVENTION: NUCLEOTIDE AND PROTEIN USA

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas CONFUTER: NY

COUNTRY: USA

ZIP: 10036/2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

COMPUTER: IBM Compatible

COMPUTER: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Manuel Pinto
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APPLICATION NUMBER: 08/981,3
FILING DATE: 22-DEC-1997
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DELTA GENE AND METHODS BASED
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                                        -QKPEC-
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.4e-178;
les 19;
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Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
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Mismatches
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FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-127
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
ORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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No. 3
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ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Amer
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         908
                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/90
FILING DATE: 17-Jul-2001
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INVENTION: NUCLEOTIDE
VERTEBRATE
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Pred.
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US-09-908-322-2
; Sequence 2, Application US/09908322
; Patent No. 6783956
; GENERAL INFORMATION:
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TYPE: amino acid
STRANDEDNESS: <Unknown>
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larity 76.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
                                                                                                                                       -SEEKAL-
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                                        FPW-AVCAGLVL-
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  NUCLEOTIDE AND PROTEIN SEQUENCES
OF VERTEBRATE DELTA GENES AND METHODS
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1.4e-178;
les 19;
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Pred. No. 3.4e
9; Mismatches
TITLE OF INVENTION: NUCLEOTIDE AND PROBLICE OF INVENTION: OF VERTEBRATE DELYNUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                    CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-038
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                     SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,392
FILING DATE: 22-DEC-1997
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nilarity 76.0%;
Conservative
                                                                                                                                MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 728 amino acids
TYPE: amino acid
                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Disker
COMPUTER: IPP
                                                                                                                                                                                                                                                                                                           212-869-8864
5141 PENNIE
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                                                                                                                                                                                                                                                                                                                                                                                                  unknown
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Best Local Similarity
Matches 546; Conser
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TOPOLOGY: ul
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                                                             STREET:
CITY:
STATE:
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US-08-872-855-8

US-08-872-855-8

Sequence 8, Application US/08872855

Patent No. 6121045

APPLICANT: McCarthy, Sean
APPLICANT: Gearing, David
TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
TITLE OF INVENTION: HONG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,855
FILING DATE: 11-UTN-1997
CLASSIFICATION: 514-1997
ATTORNEY/AGENT INFORMATION:
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                                                                                        Score 2488.5; DB Pred. No. 3.7e-178 9; Mismatches 19
REGISTRATION NUMBER: 35,430
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MAA-003.02
TELECOMMUNICATION INFORMATION:
TELEFAX: 617-832-7000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 729 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-872-855-8
                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
US-08-981-392-12
; Sequence 12, Application US/089813
; Patent No. 6262025
; GENERAL INFORMATION:
                                                                                        y Match
Local Similarity 75.9%;
hes 546; Conservative
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AND METHODS
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                           RESULL ,
US-09-908-322-12
; Sequence 12, Application US/09908322
; Patent No. 6783956
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; Henrique, Domingos Manuel Pi
; Lewis, Julian Hart
; Artavanis-Tsakonas, Spyridon
                                                                                                                                                                                                                                                                                                                                                                                                                                                Spyridon
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SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>
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FILING DATE: 22-DEC-1997
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REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
ORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 722 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                               --SSIGATOIKNTNKK-DFHDK--
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INVENTION: NUCLEOTIDE
VERTEBRATE
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TER READABLE FORM:
MEDIUM TYPE: Diskette
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APPLICANT: Ish-Horowicz, David
APPLICANT: Henrique, Domingos Manuel Pinto
APPLICANT: Lewis, Julian Hart
APPLICANT: Lewis, Julian Hart
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Gray, Grace
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASI
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
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Pred. No. 3.5e-176;
; Mismatches 24;
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                                                                                                                 SEE: Pennie & Edmonds LLP: 1155 Avenue of the Americas New York
                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-038
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,392
FILING DATE: 22-DEC-1997
CLASSIFICATION: 514
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                                                                                                                                                                         COUNTRY: C...
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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Best Local Similarity 75.9%;
Matches 548; Conservative
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MOLECULE TYPE:
8-981-392-12
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CITY: Ne
STATE: N
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                                                             Version
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Pred. No. 1.4e
6; Mismatches
STATE: MA

COUNTRY: USA

ZIP: 02109-2170

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,855
FILING DATE: 11-JUN-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MAA-003.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELECOMMUNICATION INFORMATION:
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 720 amino acids
TYPE: amino acid
TYPE: amino acid
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Best Local Similarity 76.4%;
Matches 551; Conservative
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| DVSVSIIGATQIKNTNKKADFHGDHGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHSK
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                   Score 2462; DI
Pred. No. 3.5e-
6; Mismatches
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US-08-872-855-4
; Sequence 4, Application US/08872855
; Patent No. 6121045
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean
APPLICANT: Gearing, David
; TITLE OF INVENTION: THERAPEUTIC US
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT I
; STREET: One Post Office Square
; CITY: Boston
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                   / Match
Local Similarity 75.9%;
les 548; Conservative
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                                                              DDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFVCDEHYYGEGCSVFC
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Pred. No. 1.2e-171;
11; Mismatches 27;
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US-09-068-740A-9

Sequence 9, Application US/09068740A

Patent No. 6337387

GENERAL INFORMATION:

APPLICANT: SAKANO, SELJI

APPLICANT: ITOH, AKIRA

TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVI

FILE REFERENCE: KP-8447

CURRENT APPLICATION NUMBER: US/09/068,740A

CURRENT FILING DATE: 1998-06-18

PRIOR APPLICATION NUMBER: JP 7-299611

PRIOR FILING DATE: 1995-11-17

PRIOR FILING DATE: 1995-11-17

PRIOR FILING DATE: 1996-11-15

NUMBER OF SEQ ID NOS: 48

SOFTWARE: PatentIN Ver: 2.1

SEQ ID NO 9

LENGTH: 723

LENGTH: 723
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; ORGANISM: Homo sapiens
US-09-068-740A-9
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Best Local S
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ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,855
FILING DATE: 11-JUN-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: 35,430
REFERENCE/DOCKET NUMBER: 35,430
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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Pred. No. 4.2e-175;
); Mismatches 29;
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Patent No. 6121045
GENERAL INFORMATION:
APPLICANT: McCarthy, Sean
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ADDRESSEE: FOLEY, HOAG &
STREET: One Post Office S
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Best Local Similarity 75.7%;
Matches 540; Conservative
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INFORMATION FOR
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CITY: BO
STATE: M.
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Sequence 346 Application US/10140002

Patent No. 6725730

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen
APPLICANT: Beresini, Maureen
APPLICANT: Beroyers, Luc
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gaodwaki, Paul J.

APPLICANT: Goddard, Audrey
APPLICANT: Goddwaki, Paul J.

APPLICANT: Goddwaki, Paul J.

APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Shewart, Timothy A.

APPLICANT: Stewart, Timothy A.

APPLICANT: 
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Pred. No. 1.2e-171;
; Mismatches 27;
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US-09-423-753-27

US-09-423-753-27

Sequence 27, Application US/09423753

Patent No. 6664098

GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: KP-8693

CURRENT APPLICATION NUMBER: US/09/423,753

CURRENT FILING DATE: 1999-12-30

PRIOR APPLICATION NUMBER: PCT/JP98/02104

PRIOR APPLICATION NUMBER: JP 9/124064

PRIOR FILING DATE: 1998-05-13

PRIOR FILING DATE: 1997-05-14

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin Ver: 2.1
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llarity 75.1%;
Conservative
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LENGTH: 723
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APPLICANT: SAKANO, SEIJI
APPLICANT: ITOH, AKIRA
ITTLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POI
FILE REFERENCE: KP-8447
CURRENT APPLICATION NUMBER: US/09/068,740A
CURRENT FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: JP 7-299611
PRIOR FILING DATE: 1995-11-17
PRIOR FILING DATE: 1995-11-30
PRIOR FILING DATE: 1995-11-15
                     4;
                    Score 2401.5; DB 4
Pred. No. 1.2e-171;
; Mismatches 27;
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                                 11;
                    Query Match
Best Local Similarity 75.1%;
Matches 534; Conservative
 Sapien
; ORGANISM: Homo US-10-140-002-346
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US-09-068-740A-4
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Pred. No. 8.2e-171;
; Mismatches 26;
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US-09-641-612-6
i Sequence 6, Application US/09641612
j Patent No. 6703221
j GENERAL INFORMATION:
i APPLICANT: Vivien Chan et al.
i TITLE OF INVENTION: NOTCH RECEPTOR LIGANDS AN:
FILE REFERENCE: PPO-1602.002 / 200130.498
i CURRENT APPLICATION NUMBER: US/09/641,612
i CURRENT FILING DATE: 2000-08-17
i NUMBER OF SEQ ID NOS: 10
i SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                       GVFELKLOEFVNKKGLL-NRNCCRGG--
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                                                                 Query Match
Best Local Similarity 75.4%;
Matches 529; Conservative
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Pred. No. 2.9e-161
39; Mismatches 47
                                                                                                                              NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-038
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-790-9090
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 amino and TYPE: amino and TYPE: amino and TYPE:
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                                                                                                SOFTWARE: FastSEQ Version 2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/90
FILING DATE: 22-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 68.7%;
Matches 489; Conservative
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                                               X: USA
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MOLECULE TYPE:
-981-392-5
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         ADDRESSEE:
STREET: 1
CITY: New
                                               COUNTRY:
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OF VERTEBRATE DELTA GENES AND METHODS
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                                                                 Length
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                                                               Score 2380.5; DB 4
Pred. No. 4.4e-170;
; Mismatches 30;
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US-08-981-392-5
; Sequence 5, Application US/08981392
; Patent No. 6262025
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; APPLICANT: Henrique, Domingos Manuel Pinto
; APPLICANT: Lewis, Julian Hart
; APPLICANT: Artavanis-Teakonas, Spyridon
; APPLICANT: Artavanis-Teakonas, Spyridon
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN
; TITLE OF INVENTION: OF VERTEBRATE DELTA GE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
                                                                                11;
                                                               / Match
Local Similarity 74.7%;
nes 531; Conservative
                                      sapiens
         SEQ ID NO 6
LENGTH: 723
TYPE: PRT
ORGANISM: HOMO 8
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Search completed: November 29, Job time: 19.1897 secs

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US-10-731-741-4
US-09-908-322-12
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US-09-783-931-12
US-10-417-719-4
US-10-417-719-5
US-10-042-865-108
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GENERAL INFORMATION

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GENERAL INFORMATION

MUMBER OF SEQUENCES; 94

CORRESPONDENCES: 94

CORRESPONDENCES: 94

CORRESPONDENCES: 94

CONTRY: USA

ZIP: 10036/2711

COMPUTER: READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: THE CORPETION: OUNCAND:

MEDIUM TYPE: Diskette

COMPUTER: TEM Compatible

OPERATION: OUNCAND:

MEDIUM TYPE: Diskette

COMPUTER: TEM Compatible

OPERATION: OUNCAND:

MEDIUM TYPE: Diskette

COMPUTER: TEM Compatible

OPERATION: OUNCAND:

MEDIUM TYPE: Diskette

COMPUTER: TEM Compatible

OPERATION SYSTEM OF SIDE

FILING DATE: 17-Jul-2001

CLASSIFICATION NUMBER: 08/991,392

FILING DATE: 22-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: MARIOCK, S. Leelie

NEGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1336-123
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Pred. No. 3e-238;
Mismatches 0;
             cas
                                                                                                                                                                                                                          -122
                                      COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/783,931
FILING DATE: 15-Feb-2001
CLASSIFICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-122
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
SOURNICE CHARACTERISTICS:
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TYPE: amino acid
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 ADDRESSEE: Pennie & F
STREET: 1155 Avenue c
CITY: New York
STATE: NY
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Best Local Similarity 100.0%;
Matches 578; Conservative (
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MOLECULE TYPE: peptide;
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SEQUENCE DESCRIPTION: {
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NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
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US-09-783-931-13
; Sequence 13, Application US/09783931
; Publication No. US20030073620A1
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; Henrique, Domingos Manuel Pi;
; Henrique, Joulian Hart
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
Artavanis-Tsakonas, Spyridon
Grace
                                                                                                                    13
                                                                          STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO:
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-790-9090
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 578 amino acids
TYPE: amino acid
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Best Local Similarity 100.0%;
Matches 578; Conservative (
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US-09-783-931-2
; Sequence 2, Application US/09783931
; Publication No. US20030073620A1
; GENERAL INFORMATION:
; APPLICANT: ISh-Horowicz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
Gray, Grace
; TITLE OF INVENTION: ANTIBODIES TO VERTEBRA
AND FRAGMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA

ZIP: 10036/2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/783,93:
FILING DATE: 15-Feb-2001
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Antler, Adriane M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Edmonds of the A
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & E
STREET: 1155 Avenue o
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DELTA GENE AND METHODS BASED
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.6e-173;
es 19;
                                 Pinto
                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-123
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                 Edmonds LLP
of the Americas
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Pred. No. 5.6e
9; Mismatches
                                                                                                                                                                 Henrique, Domingos Manuel
Lewis, Julian Hart
Artavanis-Tsakonas, Spyrid
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FILING DATE: 22-DEC-1997
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INVENTION: NUCLEOTIDE
VERTEBRATE
                                                                                                                                                         David
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                                                                                       RESULT 3
US-09-908-322-2
; Sequence 2, Application US/09908322
; Patent No. US20020107194A1
; Patent INFORMATION:
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ADDRESSEE: Pennie &
STREET: 1155 Avenue
CITY: New York
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76.0%;
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ULE TYPE: protein
NCE DESCRIPTION: (
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16; Conservative
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SEQUENCE
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                                                                                                                                                                      Score 2488.5; DB 1, Pred. No. 6.1e-173; ; Mismatches 19;
                          THEREOF
                          USES
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APPLICANT: Millennium Pharmaceuticals, Ir.
APPLICANT: McCarthy, Sean
APPLICANT: Gearing, David
TITLE OF INVENTION: HUMAN DELTA3 AND USES
FILE REFERENCE: MBIO1997-002CP2M
CURRENT APPLICATION NUMBER: US/10/417,719
CURRENT FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: US/09/568,218
PRIOR APPLICATION NUMBER: 08/872,855
PRIOR APPLICATION NUMBER: 08/832,633
PRIOR FILING DATE: 1997-04-04
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 4.C
SEQ ID NO 8
LENGTH: 729
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Local Similarity 75.9%;
nes 546; Conservative
                                                                                                                                           ; ORGANISM: Gallus Gallus
US-10-417-719-8
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es 19;
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         TELECOMMUNICATION INFORMATION
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
    REFERENCE/DOCKET NUMBER:
                                                                                                ΩI
                                                        LENGTH: 728 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
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US-10-417-719-8
; Sequence 8, Application US/1041771;
; Publication No. US20030180784A1
; GENERAL INFORMATION:
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                                                                                                                      Query Match
Best Local Similarity 76.0%;
Matches 546; Conservative
                                                                              TOPOLOGY: unknown MOLECULE TYPE: protein SEQUENCE DESCRIPTION: (4.783-931-2)
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CURRENT APPLICATION NUMBER: 60/260,417
PRIOR APPLICATION NUMBER: 60/260,831
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-02-28
PRIOR PILING DATE: 2001-02-28
PRIOR PILING DATE: 2001-02-28
PRIOR PILING DATE: 2001-03-29
PRIOR PILING DATE: 2001-03-29
PRIOR PILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/274,876
PRIOR PILING DATE: 2001-03-28
PRIOR PILING DATE: 2001-03-10
PRIOR PILING DATE: 2001-03-10
PRIOR PILING DATE: 2001-03-10
PRIOR PILING DATE: 2001-03-10
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:.6e-171;
les 19;
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Pred. No. 2.6e
6; Mismatches
                       Sequence 107, Application US/10042865 Publication No. US20040029216A1 GENERAL INFORMATION:
                                                                                     Zerhusen, Bryan D
Casman, Stacie J
Shenoy, Suresh G
Spytek, Kimberly
Zhong, Mei
Gangolli, Esha A
Burgess, Catherine E
Patturajan, Meera
Vernet, Corine A.M
Taylor, Sarah
Tchernev, Velizar T
Miller, Charles E
Guo, Xiaojia
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ID NO 107
SNGTH: 722
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US-10-731-741-4

Sequence 4, Application US/10731741

Publication No. US20040171148A1

GENERAL INFORMATION:

APPLICANT: Schmitt, Thomas M.

APPLICANT: Zuniga-Pflucker, Juan-Carlos

TITLE OF INVENTION: Cell Preparations Comprising Cells of

TITLE OF INVENTION: Lineage and Methods of Making and Usi;

FILE REFERENCE: 2223-171

CURRENT APPLICATION NUMBER: US/10/731,741

CURRENT FILING DATE: 2003-12-10

PRIOR FILING DATE: 2002-12-10

NUMBER OF SEQ ID NOS: 50

SOFTWARE: PatentIn version 3.1

SEQ ID NO 4

SEQ ID NO 4
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2.6e-171;
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Pred. No. 2.6e
6; Mismatches
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Pred. No. 5.2e-171;
6; Mismatches 24;
 APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-123
TELEFAX: 212-869-8864
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82
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                                                                                                                                                                                            TOPOLOGY: unknown;

MOLECULE TYPE: protein;

SEQUENCE DESCRIPTION: SEQ ID
US-09-908-322-12
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Best Local Similarity 75.9%;
Matches 548; Conservative
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AND METHODS BASED
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CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
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US-09-908-322-12
; Sequence 12, Application US/099002--
; Patent No. US20020107194A1
; GENERAL INFORMATION:
; APPLICANT: ISh-Horowicz, David
; Henrique, Domingos Malentary Henrique, Julian Hart
Artavanis-Tsakonas, S
Grace
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ZIP: 10036/2711

PUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2
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                                                                     LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFVCDE
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Pred. No. 2e-170,
6; Mismatches :
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Sequence 4, Application US/10417719

Publication No. US20030180784A1

GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: McCarthy, Sean
APPLICANT: Gearing, David
TITLE OF INVENTION: HUMAN DELTA3 AND USES TH
FILE REFERENCE: MBIO1997-002CP2M
CURRENT APPLICATION NUMBER: US/10/417,719
CURRENT FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: US/09/568,218
PRIOR FILING DATE: 1997-06-11
PRIOR FILING DATE: 1997-04-04
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 720
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Best Local Similarity 76.4%;
Matches 551; Conservative
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TYPE: PRT
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APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-122
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-869-8864
TELEFX: 66141 PENNIE
TELEX: 66141 PENNIE
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                        Edmonds LLP
of the Americas
                                                                                                                                                                                                  Spyridon
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Pred. No. 5.2e
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/783,931
    FILING DATE: 15-Feb-2001
    CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                        Henrique, Domingos Manuel P
Lewis, Julian Hart
Artavanis-Tsakonas, Spyrido
Gray, Grace
F INVENTION: ANTIBODIES TO VERT
AND FRAGMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO: 12
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
                                                                                                 RESULT 9
US-09-783-931-12
; Sequence 12, Application US/09783931
; Publication No. US20030073620A1
; GENERAL INFORMATION:
APPLICANT: ISh-Horowicz, David
Henrique, Domingos M
                                                                                                                                                                 David
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ZIP: 10036/2711
UTER READABLE FORM:
MEDIUM TYPE: Diskette
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ADDRESSEE: Pennie &
STREET: 1155 Avenue
CITY: New York
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75.9%;
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MOLECULE TYPE: protein;
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SEQUENCE DESCRIPTION: {
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STRANDEDNESS:
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INFORMATION FOR S
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                                               Score 2447.5; DB Pred. No. 5.8e-170; Mismatches 29
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Sequence 108, Application US/10042869

Publication No. US20040029216A1

GENERAL INFORMATION:

APPLICANT: Padigaru, Muralidhara

APPLICANT: Li, Li

APPLICANT: Zerhusen, Bryan D

APPLICANT: Zerhusen, Bryan D

APPLICANT: Shenoy, Suresh G

APPLICANT: Shenoy, Suresh G

APPLICANT: Shenoy, Mei

APPLICANT: Zhong, Mei

APPLICANT: Burgess, Catherine E
                                                               6
                                               Query Match
Best Local Similarity 75.7%;
Matches 540; Conservative
                           <u>8</u>
SEQ ID NO 5
LENGTH: 713
; TYPE: PRT
: ORGANISM: Rattus N
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                          , ORGANISM:
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Publication No. US20030180784A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: McCarthy, Sean
APPLICANT: Gearing, David
TITLE OF INVENTION: HUMAN DELTA3 AND USES 7
FILE REFERENCE: MBIO1997-002CP2M
CURRENT APPLICATION NUMBER: US/10/417,719
CURRENT FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: 08/872,855
PRIOR FILING DATE: 1997-06-11
PRIOR FILING DATE: 1997-06-11
PRIOR FILING DATE: 1997-04-04
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 4.0
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RESULT 13
US-09-828-366-21
; Sequence 21, Application US/09828366
; Patent No. US20020010137A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Goddard, Audrey
; APPLICANT: Glarney, Austin L.
; APPLICANT: Klein, Robert D.
; APPLICANT: Wood, William I.
; PTILE OF INVENTION: METHODS AND COMPOSITIONS FOR INF.
; TITLE OF INVENTION: CELL GROWTH
; FILE REFERENCE: P1694R1C1
; CURRENT APPLICATION NUMBER: US/09/828,366
; CURRENT FILING DATE: 2001-04-05
; Prior filing data removed - refer to PALM or file winder of SEQ ID NO 21
; LENGTH: 723
; TENGTH: 723
; LENGTH: 723
                                                                                                                                                                                                                  ATQIKNTNKK-DFH----DK---KVRYP-VDYNLV----
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1 Similarity 75.1%;
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Pred. No. 4e-169;
11; Mismatches 29;
                                      APPLICANT: Taylor, Saran
APPLICANT: Tchernev, Velizar T
APPLICANT: Miller, Charles E
APPLICANT: Guo, Xiaojia
APPLICANT: Guo, Xiaojia
APPLICANT: Garlach, Valerie L
APPLICANT: Garlach, Valerie L
APPLICANT: Edinger, Shlomit R
APPLICANT: Edinger, Shlomit R
APPLICANT: Edinger, Shlomit R
APPLICANT: Balenberg, Mark E
APPLICANT: Balenberg, Mark E
APPLICANT: Millet, Isabelle
APPLICANT: Gunther, Erik
APPLICANT: Smithson, Glennda
APPLICANT: Shone, David
TITLE OF INVENTION: Using the Same
TITLE OF INVENTION: Using the Same
TITLE OF INVENTION NUMBER: 60/260,417
PRIOR APPLICATION NUMBER: 60/260,417
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-03-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
 Patturajan, Meera
Vernet, Corine A.M
Taylor, Sarah
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illarity 75.4%;
Conservative 1
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NO 108
TH: 714
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538; Conserv
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APPLICANT:
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         VCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPAGFSGFNCEKKIDLCSSSPCSNGAKCV
                              VSRCEH-PCHNGATCHRR----YCECA-GYGG-NCQFLLPEPPGPV----DEEQFPW-AV
                                                  CAGLV---LLLLGCAA-VVCVRLK----QKP--EC--ETETMNNLANCQREKD---SSIG
                                                        -- TKVHKKC---
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RPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKPGECKCRVGWQGR
                                              578
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APPLICANT: Beresini, Maureen
APPLICANT: Desnoyers, Laura
APPLICANT: Desnoyers, Laura
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Garitsen, Mary E.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gruney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timothy A.
APPLICANT: Watanabe, Colin K
APPLICANT: Stewart, Timothy A.
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Stewart, Timothy A.
APPLICANT: Wood, William
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Wo
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Publication No. US20030004311A1
GENERAL INFORMATION:
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US-10-028-072-346
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   VL---LLLGCAA-VVCVRL---KQKPEC----ETETMNNLANCQREKD---SS
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Sequence 9, Application US/09995593A

GENERAL INFORMATION:
APPLICANT: SAKANO, SELJI
APPLICANT: ITOH, AKIRA
TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POI
FILE REFERENCE: KP8447DIV
CURRENT APPLICATION NUMBER: US/09/995,593A

CURRENT APPLICATION NUMBER: US/09/995,593A

CURRENT FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-11-17
PRIOR FILING DATE: 1995-11-17
PRIOR FILING DATE: 1995-11-17
PRIOR FILING DATE: 1996-11-30
PRIOR FILING DATE: 1996-11-15
PRIOR FILING DATE: 1996-11-15
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Pred. No. 1.3e-166;
11; Mismatches 27;
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Best Local Similarity 75.1%;
Matches 534; Conservative
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SOFTWARE: Patentin V
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US-09-995-593A-9
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PRIOR PAPLICATION NUMBER: 60/059184
PRIOR APPLICATION NUMBER: 60/059263
PRIOR PELLING DATE: 1397-09-17
PRIOR PELLING DATE: 1397-09-18
PRIOR PELLING DATE: 1397-09-19
PRIOR PELLING DATE: 1397-0-10-17
PRIOR PELLING DATE: 1397-10-17
PRIOR PELLING DATE: 1397-10-13
PRIOR PELLING DATE: 1397-10-17
PRIOR PELLING DATE: 1397-10-17
PRIOR PELLING DATE: 1397-11-12
PRIOR PELLING DATE:

PRIOR APPLICATION NUMBER; 60/074092
PRIOR FILING DATE: 1998-0-2-09
PRIOR FILING DATE: 1998-0-2-09
PRIOR FILING DATE: 1998-0-3-12
PRIOR PELICATION NUMBER; 60/079294
PRIOR PELICATION NUMBER; 60/079294
PRIOR PELING DATE: 1998-0-3-12
PRIOR PELING DATE: 1998-0-3-12
PRIOR APPLICATION NUMBER; 60/091294
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PRIOR APPLICATION NUMBER; 60/091294
PRIOR APPLICATION NUMBER; 60/091299
PRIOR APPLICATION NUMBER; 60/09139
PRIOR APPLICATION NUMBER; 60/09139
PRIOR PELING DATE: 1998-04-15
PRIOR PELING DATE: 1998-04-15
PRIOR PELING DATE: 1998-04-15
PRIOR PELING DATE: 1998-04-15
PRIOR PELING DATE: 1998-05-17
PRIOR PELING DATE: 1998-05-10
PRIOR

67	56	111	167 192	220	312	327 372	376 432	425	467 552	512 612	542 672	
ory Match st Local Similarity 75.1%; Pred. No. 1.3e-166; ches 534; Conservative 11; Mismatches 27; Indels 139; Gaps	7 SALLCVSGVFELKLQEFVNKKGLL-NRNCCRGGGCCTFFRVCLKHYQASVS !	57 PEPPCTYGSA-TPVLGSFS-PDGAG-DPAFSNPIRFPFGFTWPGTFSLIIEALHTDSP 1	112 DDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFVCDEHYYGEGCSVFC	168 RPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCD-QHG-CDKPGECKCRVGWQGR 2	221 YCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NGATCTNTGQGSY 2	280 TCSCRPGYTGCEEECPCKN-GSCTDLESSCTCPPGFYGK-CELSAMTCAD 3 13 TCSCRPGYTGATCELGIDECDPSPCKNGGSCTDLENSYSCTCPPGFYGKICELSAMTCAD 3	328 GPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKKDCSSPC-NGA-CVDLGNSY-C-CQ 3	377 AGF-GR-C-DNVDDCA-SPC-NGGTCDVND-SCTCPPGY-GKNCS-PVSRCEH-PCHN 4	426 GATCHRRYCECA-GYGG-NCQFLLPE-PPGPVDEEQFPW-AVCAGL 4	468 VLLLLGCAA-VVCVRLKQKPECETETMNNLANCQREKDSSIGATQI E	513 KNTNKK-DFHDKKVRYP-VDYNLVLKVHKKCS E	543 EEKALRKRP-SVYSTSKDTKYQSVYVSEKDEC-IATEV 578

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Search completed: November 29, 2004, 13:42:04 Job time : 62.226 secs

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2004, 13:16:29 November 29, Run on:

; Search time 14.4855 (without alignments) 3839.238 Million cell

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US-09-783-931-13 3383 score: Title: Perfect sc Sequence:

>DIKYQSVYVSEKDECIATE MGRLLASALLCVSGVFELKL.

BLOSUM62 Gapop 10.0 , Scoring table:

Gapext

0.5

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
1: pir4: * H 0 E 4

printed . No. is the number of results predicted by chance to have e greater than or equal to the score of the result being pris derived by analysis of the total score distribution. score gand is Pred

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ALIGNMENTS

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PID:98824
RESULT 1

150719
C_Delta-1 - chicken
C_Species Gallus gallus (chicken)
C; Species Gallus gallus (chicken)
C; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C; Accession: 150719
R; Henrique, D.; Adam, J.; Myat, A.; Chitnis, A.; Lewis, J.; Ish-Horowicz, D. Nature 375, 787-790, 1995
A; Title: Expression of a Delta homologue in prospective neurons in the chick. A; Reference number: 150719; MUID:95319507; PMID:7596411
A; Reference number: 150719; MUID:95319507; PMID:7596411
A; Reference number: 150719, MUID:95319507; PMID:7596411
A; Reference number: 150719, MUID:95319507; PMID:7596411
A; Reference number: 150719, MUID:95319507; PMID:7596411
A; Reference number: 150719; MUID:95319507; PMID:7596411; PMID:7504411; P
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65, 102 130 158 190 310 250 270 318 370 48 70 KCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NGAT Gaps 144; 728 Indele Length ; DB 2; 1.1e-145; nes 19; Score 2489; Di Pred. No. 1.1e-9; Mismatches 9; 73.6%; ilarity 76.0%; Conservative Query Match Best Local Similarity Matches 546; Conser 49 71 103 131 159 191 212 251 311 271 g ð 요 셤 ద g g à ò ઠે ò ò

369

ELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDL

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RESULT 3
JC7570
Delta-4 protein - human
Cispecies: Homo sapiens (man)
CiDate: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
CiAccession: JC7570
CiAccession: JC7570
CiAccession: JC7570
CiAccession: JC7570
CiAccession: JC7570
Miritle: Molecular cloning of Delta-4, a new mouse and human notch ligand.
AiTitle: Molecular cloning of Delta-4, a new mouse and human notch ligand.
AiTitle: Molecular cloning of Delta-4, a new mouse and human notch ligand.
AiTitle: Molecular cloning of Delta-4, a new mouse and human notch ligand.
AiMolecule type: mRNA
AiResidues: J-685 < YON>
AiMolecule type: mRNA
AiResidues: J-685 < YON>
AiCross-references: UNIPROT:QPNR61; DDBJ:AB043894
CiComment: This protein, a member of the Notch family of proteins, is a transmembrane recates the Notch signaling, the growth or differentiation of vascular endothelial cells.
CiGenetics:
AiGene: delta-4
CiSuperfamily: delta-4 protein; EGF homology
CiKeywords: transmembrane protein
                                                                              458
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                                      SGVFELKLOEFVNKKGLL--NRNCCRGGGCCTFFRVCLKHYQASVSPEPPCTYGS-ATPV
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             VCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCGSSPCSNGAKCV
                                                                                                                      --FPW-AVCAGLV---LLLLLGCAA-VVCVRLK-QK----PE-C--ETETMINLANCQREK
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Pred. No. 1.6e-74;
81; Mismatches 154;
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Best Local Similarity 46.4%;
Matches 314; Conservative 8
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OY 210 ECKCRVGWQCRYCDECIRYPGCVHGTCQOPWQCNCQEGWGGLPCNQDLNYCTHHRPC-NG 268	Db 185 DLNYYGSGCAKTCRPDDSFGHSTCSETGELICLTGWQGDYCHIPKCAKGCEHGHCDKBN 244 Cy 210 ECKCRVGWQGRYCDECIRYPGCYHGTCGQPWQCNCQEGWGGLECNQDLNYCTHHKPC-NG 268 1
RESULT 6 Autorea Delta Delta precursor - fruit fly (Drosophila melanogaster) C.Species Drosophila melanogaster C.Species Drosophila melanogaster C.Date: 31-War-1990 #sequence_revision 31-Mar-1990 #text_change 02-Aug-2002 C.Accession: A11246 Expecies Delta, a Drosophila melanogaster C.Accession: A11246 Expecies Delta, a Drosophila meurogenic gene, is transcriptionally complex and encodes a A.Recescence number: A31246; MUID: 89196890; PMID: 3149249 Expecience number: A31246; PMID: 3149249 Expecience number: A31246; MUID: 89196890; PMID: 3149249 Expecience number: A31246; MUID: 89196890; PMID: 31492490 Expecience number: A31246; PMID: 31492490 Expecience number: A31246, PMI	RESULT 7 S00670 Nulterrate names: gene D1 protein precursor - fruit fly (Drosophila melanogaster) NiAlterrate names: gene D1 protein NiAlterrate names: gene D1 protein C5pecies: Drosophila melanogaster C6pecies: Drosophila melanogaster C7 Date: 310-2004 C7 Accession: S00670 A7 DEGENERAL S00670 A

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DC-ASPC-NGGTC-DVNDSCTCPPGY-GKNCS-PVSRCEH-PCHNGATCH 4		CFNGGRCDNPDGGYCCPLG-SGFNCEKKDC-SSPCNGACVDLGNSYCCQAGF
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or - rat egicus (Norway rat) equence_revision 28-Apr-1995 #text_change 21-Jul-2003 ber, C.J.; Boulter, J.; Weinmaster, G. malian ligand that activates Notchl. 6136; MUID:95211842; PMID:7697721 N> 1.138483 homology <egf1> homology <egf2> 27.7%; Score 935.5; DB 2; Length 1220; y 38.4%; Pred. No. 4.1e-50; rvative 64; Mismatches 159; Indels 119; GapsVSGVFELKLQEFVNKKG-LLNRNCCRGG</egf2></egf1>	. 4 W	VLIAVESVAMPLVAVIAAC-VVFCMKRKRKRAQEKDNAEARKQNEQNAVTMHHN 6
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5 LASALLCCGTF	Query Matc Best Local Matches 2	27.7%; Score 935.5; DB 2; Length 1220; Similarity 38.4%; Pred. No. 4.1e-50; 3; Conservative 64; Mismatches 159; Indels 119; Gaps
16 DELALCALKAKVCGASGQFEDEILSMQNVNGELQNGNCCAEPGTLVKPYKCTRDECDTY 44 FRVCLKHYQASVSPEPPCTYGS-ATPVLGSFSPDGAGDPAFSNPIRFPFGFTWPGT		LASALLCVSGVFELKLQEFVNKKG-LLNRNCCRGGGCCTF

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gene serate protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Decies: Drosophila melanogaster
C;Dete: 11-Dec-1991 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C;Accession: S16149; S16879; A3666
R;Thomas, U.; Speicher; S.A.; Must, B.
Devalopment 111, 749-761, 1991
A;Title: The Drosophila gene Serate encodes an EGF-like transmembrane protein with a con A;Reference number: S16148; MUID:91347903; PMID:1840519
A;Reference number: S16148; MUID:91347903; PMID:1840519
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A;Residues: 1-1351, T',1353-1408 CTMO2>
A;Residues: 1-1352, T',1353-1408 CTMO2>
A;Residues: 1-13520, T',1353-1408 CTMO2>
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                                                                                                                                                                                                                                                                                                                                                                   CRVGWQGRYCDECIRYPGCVHGTCQ-QPWQCNCQEGWGGLFCNQDLNYCTHHKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -KNCS PVSRCEHPCHNGATCHRRYCECA - GY
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                                                                                                                                         #status predicted <TM1>
#status predicted <INT>
965,977,1004,1030,1150/Binding
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                                               <EG06
                                                                                                                                                                             Score 758.5; DB 2;
Pred. No. 3.4e-39;
; Mismatches 150;
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<EG09>
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<EG11>
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<EG13>
<EG14>

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EG05>
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EG07>
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 EG01>
EG02>
                                                                                                                                                                                                63;
                                                                                                                                                  1408/Domain: intracellular 96,247,331,412,452,558,739,
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illarity 31.5%;
Conservative 6
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LRPLCSQPP
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211; Conser
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F;283-316/Domain: EGF
F;319-348/Domain: EGF
F;355-388/Domain: EGF
F;395-488/Domain: EGF
F;495-526/Domain: EGF
F;652-683/Domain: EGF
F;652-683/Domain: EGF
F;652-683/Domain: EGF
F;803-834/Domain: EGF
F;803-834/Domain: EGF
F;883-914/Domain: EGF
F;997-1060/Region: CY
F;1222-1246/Domain: tr
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PID:9433 patte S42612
transmembrane protein precursor - zebra fish
C;Species Brachydanio rerio (zebra fish)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S42612
R;Bierkamp, C.; Campos-Ortega, J.A.
Mech. Dev. 43, 87-100, 1993
A;Title: A zebrafish homologue of the Drosophila neurogenic gene Notch and its F
A;Reference number: S42612; MUID:94128602; PMID:8297791
A;Reference number: S42612; MUID:94128602; PMID:8297791
A;Reference number: S42612; MUID:94128602; PMID:8297791
A;Reference number: A2612
A;Reference number: A2612
A;Redidues: 1-2437
A;Residues: numby
A;Residues: 1-2437
A;Residues: numby
A;Residues: numby
A;Residues: numby
B;1023-1054/Domain: EGF homology < EGF2>
F;1031-1054/Domain: ankyrin repeat homology < AN1>
F;1940-1980/Domain: ankyrin repeat homology < AN3>
F;2048-2080/Domain: ankyrin repeat homology < AN5>
F;2048-2080/Domain: ankyrin repeat homology < AN5> ita 48 110 316 671 409 202 148 0 282 α 791 ٦. 73 | | | | : | : | ACISNPCQKGSNCDTNPVSGKAICTCPPGYTGSACNQDIDECSLGANPCEHGGRCLNTKG CRPGYTG--CE---EEC---PCKNGSCTDLESS--CTCPPGFYGK-CELSAMTCADGPCF NGGRCDNPDGGY - - CCPLG - SGFNCEKK - - DCS - SPCN - GACVDLGNSY - - CCQAGF - - G -CVHGTC----QQPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NGATCTNTGQGSYTCS -YCEC-AGYGG-NCOFLLP --GGTCVQTSDTTHTCSCLPGFTGQTCEHN V D D C T Q H A C E N G G P C I D G I N T Y N C H C D K H W T G Q Y C T E D V D E C E L S P N A C D N G T C H N T I G --DLY GFHCVCVNGWTGDDCS---ENIDDCASAACSHGATCHDRVASFFCECPHGRTGLLCHLDD --SHYICTCPPNFHGQTCRQDVNECAVSPSPCRNGGTCINEVGSYL VLGSF SSGRT--QASVSPEPPCTYGSATP 285; 2437 -ECIRYPG-Length Ø -DPAFSNPIRFPFGFTWPGTFSLIIEALHTDS Indel --QRHLVGEEWSQDLH--•• -GKNCS - PVSRC - EHPCHNGATCHRR -, DB 2; Se-23; SB 182; -000-RCD-NVDDCA-SPC-NGGTC--DVND-SCTCPPGY--SYRFVCDEHYYGEGCSVFCRPRDDFGHFTCGRGEKC-Score 496.5; Pred. No. 6.5e 64; Mismatches

	Oy 493	embrane protein F homology <egf1> GF homology <egf3> EGF homology <egf3> EGF homology <egx1> transmembrane #status predicted <tm1> 14.5%; Score 491; DB 2; Length 385; arity 32.8%; Pred. No. 3.2e-23; onservative 39; Mismatches 95; Indels 124; Gaps rcgrgercpgwkGQYCTPICLPGCD-QHG-CDKPGECKCRVGWQGRYCDECIRYPG</tm1></egx1></egf3></egf3></egf1>	231 CVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCNGATCTNTGQGSYTCSCRPGYTG- : : :	332 NGGRCDNPDGGYCCPLGSGFNCEKY : : : :	RESULT 13 A46019 notch-1: protein - mouse N; Alternate names: motch protein C; Species: Mus musculus (house mouse) C; Date: 22-Sep-1993 #sequence revision 18-Nov-1994 #text change 16-Aug-2004 C; Accession: A46019; S25144; C49175; B46438; A46438; PH1569; S32109 C; Accession: A46019; S25144; C49175; B46438; PH1569; S32109 R; del Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Copeland, N.G.; Grid Genomics 15, 259-264, 1993 A:Title: Cloning, and chromosomal localization of Notch-1, a mouse homolog of lates.
	protein - African clawed frog les: Xenopus laevis (African clawed frog) : 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 16-Aug-2004 ssion: A35844 man, C.; Harris, W.; Kintner, C. e 249, 1438-1441, 1990 e: Xotch, the Xenopus homolog of Drosophila notch. e: Xotch, the Xenopus homolog of Drosophila notch. e: Xotch, the Xenopus homolog of Brosophila notch. ssion: A35844 us: preliminary; nucleic acid sequence not shown; not compared with conceptual cule type: mRNA dues: 1-2524 <cof> rfamily: Notch protein; ankyrin repeat homology; EGF homology ords: transmembrane protein 177/Domain: EGF homology <egx1> 215/Domain: EGF homology <egf1> 254/Domain: EGF homology <egf></egf></egf1></egx1></cof>	456-487/Domain: EGF homology <egk2> 1025-1056/Domain: EGF homology <egk3> 1025-1056/Domain: EGF homology <egk3> 1924-1956/Domain: ankyrin repeat homology <an1> 1957-1989/Domain: ankyrin repeat homology <an3> 2024-2056/Domain: ankyrin repeat homology <an4> 2057-2089/Domain: ankyrin repeat homology <an5> 2057-2089/Domain: ankyrin repeat homology <an5> 2057-2089/Domain: ankyrin repeat homology <an5> 2057-2089/Domain: ankyrin repeat homology of and allowed ankyrin repeat homology of and allowed ankyrin repeat homology of an allowed ankyrin repeat homology of allowed any allowed ankyrin repeat homology of allowed ankyrin</an5></an5></an5></an4></an3></an1></egk3></egk3></egk2>		169 PRDDFGHFTCGRGEKC-PGWKGQYC-TPICLPGCDQHGCD 20	Qy 287 YTGCEEECPCKNGSCTDLESSCTCPPGFYGK-CELSAMTCADGPCFNGGR 335 b 633 TTGVNCETKIDDCASNLCDNGKCIDKIDGYECTCEPGYTGKLCNININECDSNPCRNGGT 692 Qy 336 CDNPDGGYCCPLGSGFNCEKKDC-SSPC-NGACVDLGNSY-C-CQAGFGRCD- 383 b

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Motch B protein - mouse (fragment)

N;Alternate names: Notch homolog

C;Species: Mus musculus (house mouse)

C;Accession: A49175; PH1570; $32113

C;Accession: A49175; PH1570; $32113

R;Lardelli, M.; Lendahl, U.

Exp. Cell Res. 204, 364-372, 1993

A;Title: Motch A and Motch B--two mouse Notch homologues coexpressed in a wide variety of A;Reference number: A49175; MUID:93178563; PMID:8440332

A;Accession: A49175

A;Accession: A49175

A;Accession: A49175

A;Accession: A49175

A;Residues: 1-1203 <LAR>
A;Residues: 1-1203 <LAR>
A;Residues: 1-1203 <LAR>
A;Residues: UNIPROT:035516; EMBL:X68279; NID:9287989; PIDN:CAA48340.1; PID:928799;
A;Acoss-references: embryo

A;Note: sequence extracted from NCBI backbone (NCBIP:126158)

C;Comment: This protein has many EGF repeats and lin-12/Notch repeats.
C;Comment: This protein is one of the neurogenic proteins controlling the decision betwee
                                                     50;
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--SVSCEVAAQKRGIDVTLL
                                                                                                                                      CMDKIHEFQCQ----CPKGFNGHLCQYDVDECASTPCKNGAKCLDGPNTYTCVCTEGYTGT
                                                                                                                                                                                                                                                                   -DDLTENPERLISRLTQRHLVGEEWSQDLHSSG
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                                                                                               FFRVCLKHYQAS
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                                                     Gaps
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              Length
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             DB 2;
3-22;
202;
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                                  8e-
             Score 489.5;
Pred. No. 1.8e
0; Mismatches
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                                                                                                                                                                                  -VSPEPPCTYGSATPVLGSFS--
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                                                                                               CVSGVFELKLQEFVNKKGLLNRNC-
                                                                                                                                                                                                                                                                    -LIIEALHTDSP-
                                                    201
             Query Match
Best Local Similarity 27.9%;
Matches 193; Conservative
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A49175
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Residues: 1865-1932, 'RR',1935-1937,'L',1938-1967,'I',1969-2044,'IE',2047-2052,'S'
Experimental source: embryo
Note: sequence extracted from NCBI backbone (NCBIN:131246, NCBIP:131247)
Comment: This protein has many EGF repeats and lin-12[#1172]/Notch repeats.
                                                                                                                                                               Greenspan,
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A. Reference number: A46019; WID: 93194170; PWID: 8449489
A. Retailer Compared with Conceptual translation
A. Wolters and Compared with Conceptual translation
A. Molecia Sequence extracted from NCE backbook (WCEPP.1218)
B. Franco dal Amo, F.; Saith, D. E.; Switck, P. J. Gendron-Magnire, M.;
A. Description: Expression pattern of Worth, a mouse homolog of Drosophis
A. Molecia Sequence extracted from NCE backbook (WCEPP.1218)
A. Molecia Sequence extracted from NCE backbook (WCEPP.1218)
A. Molecian Sail Amo, F.; Saith, D. E.; Switck, P. J. Gendron-Magnire, M.;
A. Molecian Sail Amo, F.; Saith, D. E.; Switck, P. J. Gendron-Magnire, M.;
A. Molecian Sail Amo, F.; Saith, D. E.; Switck, P. J. Gendron-Magnire, M.;
A. Molecian Sail Amo, F.; Saith, D. E.; Switck, P. J. Gendron-Magnire, M.;
A. M. Landahl, T. Land
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LGYTGKN
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                                                                                                                                                                                                                                                                                                                            CLNDGRCIDL----VNGYQCNCQPGTSGLNCEINPDDCASNPCMHGVCVDGINRYSCVCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -- CIHGNCTGGLSGYKCLCDAGWVGVNCEVDKNECLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CMNNGVCHNTQGSYVCECPPGFSGMDCEEDINDCLAN-PCQNGGSCVD-HVNTFSCQCHP
                                                                                                                                                                                                                                                                                                                                                                              LHTDSPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            447 NPCONGG--TCNNLVNGYRCTCKKGFKGYNCQVNIDECASNPCLNQGTCFDDVSGYTCHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DECIRYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MLPYTGKNCQTVLAPCSPNPCENAAVCKEAPNFESFSCLCAPGWQGKRCTVDVDECISKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCVHGTC---QQPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NGATCTNTGQGSYTCSCRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -CPLG-SGFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -VCVRLKQKPECETETMNNLAN-CQREK
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -CAGGPHCLNGGQCVDRIGGYTCRCLPGFAGERCEGDINECLSNPCSSE
                                                                                                                                                                                                                                                                                  - EPPCTYGSATPVLGSF
                                                                                                                                                                                                                                                                                                                                                                                                                     PGFTGORCNIDIDECASNPCRKGATCINDVNGFRCICPEGPHHPSCYSQVNECL-
                                                                                                                                                                                                                                       310;
     EGF homology
                                                                                                                                                                                                                                                                                                                                                                            - FPFGFTWPGTFSLIIEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GY-GKNCS-PVSRCEH-PCHNGATC----HRRYCECAGYGGNCQFLLPEPPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLTENPERLISRLTORHLVGEEWSQDLHSSGRTDLYSYRFVCDEHYYGEGCSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCVDGINSFSCLCPVGFTGPFCLHDINECSSNPCLNAGTCVDGLGTYRCICP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --CRVGWQGRYC---
                                                                                                                                                                                          1203;
                                                                                                                                                                                                                                      Indela
                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -DNP--DGGYC
      repeat homology
                                                                                                                                                                                         ore 485; DB 2;
ed. No. 1.9e-22;
Mismatches 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GYOGVNCEYEVDECQNOPCQNGGTCIDLVNHFKCSC-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPRDDFGHFTCG----RGEKC---PGWKGQYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---PGCDQHGCDKPGECK---
                                                                                                                                                                                          Score 485;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   notch protein homolog - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Feb-1994 #sequence_revision 10
C;Accession: S18188
R;Weinmaster, G.; Roberts, V.J.; Lemke, G
Development 113, 199-205, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -VDEEOFPWAVCAGLVLLLLGCAAV
 ankyrin

< EGX1>

< EGF1>

< EGF2>

< EGX2>

< EGX3>
                                                                                                                                                                                                                                                                              CCRGGGCCTFFRVCLKHYQASVSP
                                                                                                                                                                                                                                  59;
                                                                                                                                                                                                                                                                                                                                                                            -DPAFSNPIR
C; Superfamily: Notch protein; and F;143-174/Domain: EGF homology <| F;482-513/Domain: EGF homology <| F;560-591/Domain: EGF homology <| F;674-705/Domain: EGF homology <| F;712-743/Domain: EGF homology <| F;836-867/Domain: EGF homology <| F;836
                                                                                                                                                                                      14.3%;
Similarity 25.2%;
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        514
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                                                                                                                                                                                                                                                                                                                                                                            PDGAG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---SNP-
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                                                                                                                                                                                                                                184;
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Best Local S
Matches 184
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      development
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NGATCTNTGQGSYT
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    - KINEFLCOCPKĠFSGHLĊQYDVDECASTPĊKNĠAKĊLDGPNTYTCVĊTEGYT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCFNGGRCDNPDGGYCCPLGSGFN---CEKK--DCS-SPC--NGACVDLGNSY--CCQAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>PCQNGANCTDCVDSYTCTCPTGFNGIHCENNTPDCTESSCFNGGTCVDGINSFTCLCPPG</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --YCEC-AGYGG-NCOFLLPEPPGPVDEEQFPWAVCA---GLVLLLGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --GRCD-NVDDCAS-PC-NGGTCDVNDS-----CTCPPGY-GKNCSPVSR-CEH-PCHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -RGEKC---PGWKGQYCTPICLPGCDQHGCDKPGECK-
                                                                                                                                                                                                                                                                                                                                                                                                  2531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                239;
     mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --FCRPRDDFGHFTCG-
                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                Indele
                                                                                                                                                     EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRGGGCC
      of Drosophila Notch expressed during S18188; MUID:92111383; PMID:1764995
                                                                                                                               PID:g57635
homology;
                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
3-22;
208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDGAG-
                                                                                                                                                                                                                                                   ch 14.3%; Score 484.5; Dil Similarity 27.5%; Pred. No. 3.7e-189; Conservative 52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRVGWQGRYC----DECIRYPGCVHGTC--
A; Title: A homolog of Drosophila Notch expresses A; Reference number: $18188; MUID:92111383; PMID A; Recession: $18188
A; Molecule type: mRNA A; Residues: 1-2531 < WEI>
A; Cross-references: EMBL: X57405; NID:957634; PIC: Superfamily: notch protein; ankyrin repeat homology < EGF1>
F; 1025-1056/Domain: EGF homology < EGF2>
F; 1233-1264/Domain: EGF homology < EGF2>
F; 1950-1982/Domain: ankyrin repeat homology < AN F; 1964-2016/Domain: ankyrin repeat homology < AN F; 2017-2049/Domain: ankyrin repeat homology < AN F; 2017-2049/Domain: ankyrin repeat homology < AN F; 2050-2082/Domain: ankyrin r
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1825181 segs, 575374646 residues Searched:

1825181 of hits satisfying chosen parameters: Total number

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Database

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11 01.00V-1996 (TERMBLEE1 01, Created)
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12 01.00V-1996 (TERMBLEE1 26, Last annotation update)
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9; Mismatches 19;
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                                                                                                                                                             EMBL, X809031; CAA56865.1; -.

R HSSP, P00740, LEDM.

R INCACt, Q644834.

R INCACt, Q644834.

R GO; GO:0005587; C:extracellular; ISS.

GO; GO:0005515; F:protein binding; IPI.

GO; GO:000515; F:protein binding; IPI.

GO; GO:0001709; P:cell fate determination; ISS.

R DITCEPTO; IPRO0184; EGF_CA.

R INTERPO; IPRO0184; EGF_CA.

R INTERPO; IPRO0184; EGF_CA.

R PROSITE; PRO0101, ASY HYDROXVL; 3.

R PROSITE; PRO0101, ASY HYDROXVL; 3.

R PROSITE; PRO0104; EGF_CA.

R PROSITE; PRO0106; EGF_CA.

R PROSITE; PRO0106
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Delta-like protein 1.
Extracellular (Potential)
Potential.
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heart and at lower levels, in adult lung. DEVELOPMENTAL STAGE: Expressed until day Expression then decreases and increases simiLARITY: Contains 1 DSL domain. SIMILARITY: Contains 8 EGF-like domains.
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SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: In the embryo, expressed in the paraxial
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of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C57BL/6 X BALB/c; TISSUE=Embryo;
MEDLINE=95401858; PubMed=7671806;
MEDLINE=95401858; PubMed=7671806;
Bettenhausen B., de Angelis M.H., Simon D., Guenet J.-L., Gossle "Transient and restricted expression during mouse embryogenesis Dll1, a murine gene closely related to Drosophila Delta.";
Development 121:2407-2418(1995).
-!- FUNCTION: May be involved in cell-to-cell communication in mammalian embryos. May have a role in cellular interactions
           YGEGCSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCD-QHG-C
                                                                                                                                               KCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKP
                                                                                                                                                                                                           FPW-AVCAGLVL---LLLGCAA-VVCVRLK-----QKPEC---ETETMNNLANC
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  KHYQASVSPEPPCTYGSA-TPVLG--SFS-PDGAG--DPAFSNPIRFPFGFTWP
                                                                                                                                                                                               CTNTGOGSYTCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPG
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01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Delta-like protein 1 precursor (Drosophila Delta homolog
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Pred. No. 3.5e-172;
Mismatches 19
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SEQUENCE FROM N.A.

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STRAIN=C57BL/6; TISSUE=Mouse;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MALSCHUL S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Jordan H., Moore T., Max S. I., Wang J., Heibh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M., Soares M.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Andes S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.W., Anthalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Anthalon D.K., Marra M.A., Schmutz J., Myers R.M., Butterfield Y.S., Gones S.J., Marra M.A.;

Mones S.J., Marra M.A.;

Generation and initial analysis of more than 15,000 full-length human and minitial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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STRAIN=C57BL/6J;

Brathwaite M., Waeltz P., Dudekula D., Nagaraja R.;

Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: Contains 8 EGF-like domains.

EMBL; BC057400; AAH57400.1; -.

EMBL; BC055063; AAH65063.1; -.

EMBL; AY497019; AAR30869.1; -.

GO; GO:0007386; P:compartment specification; IMP.

GO; GO:0007386; P:compartment specification; IMP.

GO; GO:0007386; P:compartment specification; IMP.

GO; GO:0007386; P:somite specification; IMP.

GO; GO:000747; P:somite specification; IMP.

InterPro; IPR00174; DSL.

InterPro; IPR001881; EGF_2.

InterPro; IPR001438; EGF_II.

InterPro; IPR001438; EGF_II.

InterPro; IPR006209; EGF_II.
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STRAIN=C57BL/6; TISSUE=Mouse;
Strausberg R.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases
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STRAIN=C57BL/6J;
Nagaraja R., Waeltz P., Brathwaite M.E.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ
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RDTKCQSQSSAGEEKIAPTLRGGEIPDRKRPESVYSTSKDTKYQSVYVLSAEKD
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                                                                                   Score 2466; DB 2;
Pred. No. 3.5e-172;
Mismatches 19
                                                                         9D570B9DC7EEC75E
Pfam; PF01414; DSL; 1.

Pfam; PF00008; EGF; 6.

Pfam; PF07645; EGF CA; 1.

PRINTS; PR00010; EGFBLOOD.

SMART; SM00181; EGF; 8.

SMART; SM00181; EGF; 8.

SMART; SM00179; EGF CA; 6.

PROSITE; PS00010; ASX HYDROXYL; 3

PROSITE; PS01186; EGF 2; 8.

PROSITE; PS01186; EGF 2; 8.

PROSITE; PS01187; EGF 2; 8.
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SEQUENCE FROM N.A.

STRAIN=C57BL/6; TISSUE=Mouse;

KEDINE=22388257; PubMed=12477932;

KEDINE=22388257; PubMed=12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Tonne C. T. Marry M. A.

Touchman J.W. Smailus D.E., Schnerch A., Schein J.E.,
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Sciurognathi; Muridae; Musinae; Mus
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases
EMBL; BC057400; AAH57400.1; -.
SEQUENCE 722 AA; 78449 MW; 9D570B9DC7EEC75E CRC64;
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Pred. No. 3.5e-172;
6; Mismatches 19;
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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STRAIN-C57BL/6; TISSUE=Mouse
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02-MAR-2004 (TrEMBLrel.
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Proc. Natl. Acad.
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                                  DLGNSY-C-CQAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J;
Brathwaite M., Waeltz P., Dudekula D., Nagaraja R.;
Brathwaite (DEC-2003) to the EMBL/GenBank/DDBJ databases
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases
EMBL; AY497019; AAR30869.1; -.
SEQUENCE 722 AA; 78449 MW; 9D570B9DC7EEC75E CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata
Mammalia; Eutheria; Rodentia; Sciurognathi; Murida
NCBI_TaxID=10090;
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Pred. No. 3.5e-172;
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SEQUENCE FROM N.A.

STRAIN=C57BL/6; TISSUE=Mouse;

X RAINS=C57BL/6; TISSUE=Mouse;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Habeh F.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Habeh F.,

Bloomstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Kahey J., Halton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

Richeration and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
DLGNSY-C-CQAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-P
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Pred. No. 3.5e-172;
6; Mismatches 19;
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; 9D570B9DC7EEC75E
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2)
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Mouse;
Strausberg R.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ
EMBL; BC065063; AAH65063.1; -.
SEQUENCE 722 AA; 78449 MW; 9D570B9DC7EEC75
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Disiblo G., Hebshi L., Boulter J., Weinmaster G.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May be involved in cell-to-cell communication in mammalian embryos. May have a role in cellular interactions underlying somitogenesis and development of the nervous system (By similarity).
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Murinae; Rat
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Pfam; PF01414; DSL; 1.
Pfam; PF00008; EGF; 6.
PRINTS; PR00010; EGFBLOOD.
SMART; SM00179; EGF CA; 4.
SMART; SM00179; EGF CA; 4.
PROSITE; PS00012; EGF 1; 8.
PROSITE; PS01186; EGF 2; 8.
PROSITE; PS01187; EGF 2; 8.
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HSSP; P08709; 1BF9.
RGD; 70949; D111.
RGD; 70949; D111.
RGD; 70949; D111.
RGD; G0:0005576; C:extracellular; ISS.
G0; G0:000512; F:Notch binding; IPI.
G0; G0:0001701; F:Notch binding; IPI.
G0; G0:0001701; P:embryonic development (sensu Mammalia); ISG.
G0; G0:0001701; P:hair cell fate commitment; NAS.
G0; G0:0009912; P:hair cell fate commitment; NAS.
G0; G0:0009912; P:hemopoiesis; ISS.
G0; G0:0007399; P:neurogenesis; ISS.
G0; G0:0007399; P:neurogenesis; ISS.
G0; G0:0007219; P:Notch signaling pathway; NAS.
InterPro; IPR00174; EGF_2.
InterPro; IPR00174; EGF_2.
InterPro; IPR00144; EGF_1I.
InterPro; IPR001443; EGF_II.
InterPro; IPR001443; EGF_II.
InterPro; IPR001443; EGF_II.
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Delta-like protein 1.

Extracellular (Potential).

Potential.

Cytoplasmic (Potential).

DSL.
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: Interacts with Notch receptors.
SUBCELLULAR LOCATION: Type I membrane protein
SIMILARITY: Contains 1 DSL domain.
SIMILARITY: Contains 8 EGF-like domains.
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Delta-like protein 1 precursor
Name=D111;
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Rodentia; S
NCBI_TaxID=10116;
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PRT;
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                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primatea;
NCBI_TaxID=9606;
                                          STANDARD;
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MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd F.
Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
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MEDLINE=99180765; PubMed=10079256;
Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,
Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas
"Human ligands of the Notch receptor.";
Am. J. Pathol. 154:785-794(1999).
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Catarrhini; Hominidae; Homo.
                                                                     SEQUENCE FROM N.A.
Han W., Ye Q., Moore M.A.S.;
"A soluble form of human delta-like-1 inhibits differentiation hematopoietic progenitor cells.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Delta-like protein 1 precursor (Drosophila Delta homolog
(H-Delta-1) (UNQ146/PRO172).
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Oda T., Chandrasekharappa S.C.;
"Human Delta 1 gene sequence.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
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                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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  SUBCELLULAR LOCATION: Type I membrane protein.
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SIMILARITY: Contains 1 DSL domain.
SIMILARITY: Contains 8 EGF-like domains.
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Delta-like protein 1.
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Potential.
Cytoplasmic (Potential).
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EGF-like 3.
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MEDLINE=95319507; PubMed=7596411;
Henrique D., Adam J., Myat A., Chitnis A., Lewis J., Ish-Horowicz
"Expression of a Delta homologue in prospective neurons in the
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y a homologue
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X-Delta-1.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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                   23
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Craniata; Vertebrata; Euteleostor
Salamandroidea; Salamandridae; C
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databases.
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Last sequence update)
Last annotation update
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Nakamura K., Kikuchi Y., Susaki K., Chiba C., Sai Sequence K., Kikuchi Y., Susaki K., Chiba C., Sai Sumitted (OCT-2002) to the EMBL/GenBank/DDBJ data Sumitted (OCT-2002) to the EMBL/GenBank/DDBJ data submitted (OCT-2002) to the EMBL/GenBank/DDBJ data submitted (OCT-2002) contains 8 EGF-like domains.

EMBL; AB095017; BAC41350.2; -.

HSSP; P00740; IEDM.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0007154; P:callium ion binding; IEA.

GO; GO:0007154; P:callium ion binding; IEA.

InterPro; IPR00152; ABX hydroxyl_S.

InterPro; IPR001438; EGF_C.

InterPro; IPR001438; EGF_TI.

InterPro; IPR006209; EGF_II.

InterPro; IPR006209; EGF_II.

Pfam; PF001008; EGF; 6.

PROSITE; PS00010; ASX HYDROXYL; 3.

PROSITE; PS00010; ASX HYDROXYL; 3.

PROSITE; PS001186; EGF_2; 7.

PROSITE; PS01186; EGF_2; 7.

PROSITE; PS01186; EGF_CA; 2.

EGF-like domain.

SEGF-Like domain.
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Best Local Similarity 68.9%;
Matches 496; Conservative 2
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(TrEMBLrel.
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Eukaryota; Metazoa; Ch
Amphibia; Batrachia; C
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Q8AW87;
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01-MAR-2004 (Tr
Ligand Delta-1.
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PROSITE,
EGF-like
SEQUENCE
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Pred. No. 3e-144;
51; Mismatches 69;
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69;
                        of
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                         region
                            Gene.";

Bevelopment 129:4773-4784(2002).

EMBL; AF426384; AAL31528.1; -.

HSSP; P00740; 1EDM.

GO; GO:0016020; C:membrane; 1EA.

GO; GO:0005509; F:calcium ion binding; II

GO; GO:0007154; P:cell communication; IEI

InterPro; IPR00152; ABX_hydroxyl_S.

InterPro; IPR001774; DSL.

InterPro; IPR001438; EGF_2.

InterPro; IPR001438; EGF_1I.

InterPro; IPR0016209; EGF_1I.

Pfam; PF01414; DSL; 1.

Pfam; PF01414; DSL; 1.

Pfam; PF01010; EGFBLOOD.

SMART; SM00179; EGF_Z; 8.

PROSITE; PS00100; ASX_HYDROXYL; 3.

PROSITE; PS01186; EGF_Z; 8.

PROSITE; PS01186; EGF_Z; 8.

PROSITE; PS01186; EGF_Z; 8.

PROSITE; PS01187; EGF_Z; 2.

EGF-like domain.
                         atory
SEQUENCE FROM N.A.
MEDLINE=22248969; PubMed=12361969
Hans S., Campos-Ortega J.A.;
"On the organisation of the regul
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il Similarity 63.4%;
456; Conservative 5
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Q8UWJ4;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DeltaD protein.
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidae; Danio.
NCBI_TaxID=7955;
[1]
                                                                 Indels
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                                                                                LLASALLC --- VSGVFELKLQEFVNKKGLL-NRNCCRGGG
                                               Score 2262.5; DB 2
Pred. No. 2.8e-157;
); Mismatches 47;
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EGF_2; 8
EGF_3; 6
EGF_CA;
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                                                        11 Similarity 68.7489; Conservative
PS01186; E
PS50026; E
PS01187; E
domain.
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                                                                                                                                         DeltaD transmembrane protein precursor.

Name=dld; Synonyms=deltaD;

Brachydanio rerio (Zebrafish) (Danio rerio).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniform(Cyprinidae; Danio.)

NCBI_TaxID=7955;
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=97346722; PubMed=9203139;
Dornseifer P., Takke C., Campos-Ortega J.A.;
"Overexpression of a zebrafish homologue of the Drosophila neur gene delta perturbs differentiation of primary neurons and somi development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VCLKHYQASVSPEPPCTYGSA-TPVLGSFS---PDGAGDPAFSNPIRFPFGFT
                                    -ALRKRPSVYSTSKDTKYQSVYV--SEKD
 -- KVRYP-VDYNLVLKVHK
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9C5A0162504593E4 CRC64;
                                                                                                                             Last sequence update)
Last annotation update)
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Mech. Dev. 63:159-171(1997).

EMBL; Y11760; CAA72425.1; -.

HSSP; P00740; 1EDM.

ZFIN; ZDB-GENE-990415-47; dld.

ZFIN; ZDB-GENE-990415-47; dld.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0007154; P:cell communication; IEA.

InterPro; IPR00152; Asx_hydroxyl_S.

InterPro; IPR001774; DSL.

InterPro; IPR001881; EGF_Ca.

InterPro; IPR001438; EGF_II.

InterPro; IPR006209; EGF_II.

InterPro; IPR006209; EGF_II.

Pfam; PF01414; DSL; 1.

PRINTS; PR00010; EGFBLOOD.
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Pred. No. 5e-144
51; Mismatches
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PROSITE; PS00010; ASX HYDROXYL; 3.
PROSITE; PS00022; EGF_1; 8.
PROSITE; PS01186; EGF_2; 8.
PROSITE; PS50026; EGF_3; 6.
PROSITE; PS01187; EGF_CA; 2.
PROSITE; PS01187; EGF_CA; 2.
GATQIKNTNKK-DFH---DK-
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ilarity 63.4%;
Conservative 51
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SMART; SM00179; EGF_CA
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P87357;
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O1-MAY-1997
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PROSITE;
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TISSUE=Embryo;

MEDLINE=22388257; PubMed=12477932;

MAltschul S.F., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haith F.,

Mattachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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Maha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robar S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                           240
210
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Q6D148
Q6D148;
Q6D148;
Q6D148;
Q6D148;
Q1-OCT-2004 (TrEMBLrel. 28, Last sequence update)
Q1-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Q1-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Q1-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein.
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Cyprinidae; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
Cyprinidae; Danio.
NCBI_TaxID=7955;
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YGK-CELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK--DC-SSPC-NGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DeltaA.
Name=dla; Synonyms=deltaA;
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI TaxID=7955;
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Pred. No. 3.1e-137;
1; Mismatches 80;
                                                                                                                                         MEDLINE=98165392; PubMed=9425133; Appel B., Eisen J.S.; Appel B., Eisen J.S.; Regulation of neuronal specification in the zeb belta function."; Development 125:371-380(1998).

EMBL; AF030031; AAC41249.1; -. HSSP; PO0740; IEDM.
ZFIN; ZDB-GBNE-980526-29; dla.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
InterPro; IPR00182; Asx_bydroxyl_S.
InterPro; IPR00183; EGF_I.
InterPro; IPR001842; EGF_I.
InterPro; IPR001843; EGF_II.
InterPro; IPR00189; EGF_II.
InterPro; IPR00109; EGF_II.
Pfam; PF01414; DSL; 1.
Pfam; PF00109; EGF_II.
SMART; SM00051; DSL; 1.
SMART; SM00109; EGF_I; 8.
PROSITE; PS00102; EGF_I; 8.
PROSITE; PS00109; EGF_I; 8.
PROSITE; PS01187; EGF_Z; 8.
PROSITE; PS01187; EGF_Z; 8.
PROSITE; PS01187; EGF_Z; 1.
EGF_IIME GOMAIN.
EGF_IIME GOMAIN.
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                                                                                                                                                              Score 2014; DB 2;
Pred. No. 4.8e-139;
48; Mismatches 76;
                                                                                                                                    716A014158938576
                                        SEQUENCE FROM N.A.
TISSUE=Embryo;
Strausberg R.;
Strausberg R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ
EMBL; BC075742; AAH75742.1; -.
Hypothetical protein.
SEQUENCE 772 AA; 84968 MW; 716A0141589385
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11 Similarity 58.4%;
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X Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rywinski M.I., Skalbka U., Schmutz J., Myers R.M., Butterfield Y.S.,

A Krzywinski M.I., Skalbka U., Smailus D.E., Schnerch A., Schein J.E.,
                                          GYTGRNC
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Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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MEDLINE=22341132; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
"Genetic and genomic tools for Xenopus research: The NIH Xenopus
 --RCDNV-DDCAS-PC-NGGTCDVNDS---CTCPP
                      -OKPECETETMINIA-NCORE
                                                                                                                                                                                           than 15,000 full-leng
                                                                                                          ----PSVYSTSK--
                                                                                                                                                                                                                                                   -- KVRY-PVDYNLV-
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Last sequence update)
Last annotation update)
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id. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                          -- LKVHKKCSEEKALRKR
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                                                                                                                                                                   --GCA-AVVCVRLK-
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24,
  -CVDLGNSYCCOAGFG--
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hev Dvn. 225:384-391(2002)
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01-JUN-2003
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                                  databases
                                                                                                                                                                                                                                                                                                                                                            CRC64
                                                                                                                                                                                                                                                                                                                                                                                  Score 1383; DB 2;
Pred. No. 6.4e-93;
74; Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                            56AFB4013E1C2AE2
                                 EMBL/GenBank/DDBJ
                                                                                     ; IEA.
Klein S., Strausberg R.;
Klein S., Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank
EMBL; BC044262; AAH44262.1; -.
HSSP; P00740; 1EDM.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005509; F:calcium ion binding; I
GO; GO:0007154; P:cell communication; IEI
InterPro; IPR00152; ABX_hydroxyl_S.
InterPro; IPR00174; DSL.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR006209; EGF_II.
InterPro; IPR006209; EGF_II.
Pfam; PF01414; DSL; 1.
Pfam; PF00109; EGF_CA; 1.
Pfam; PF0010; EGFELOOD.
SMART; SM00179; EGF_CA; 1.
PROSITE; PS0010; ASX_HYDROXYL; 2.
PROSITE; PS001186; EGF_2; 7.
PROSITE; PS001187; EGF_CA; 2.
PROSITE; PS001187; EGF_CA; 2.
EGF-Iike domain.
SEQUENCE 642 AA; 70655 WW; 56AFB4013
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Local Similarity 46.3%;
hes 310; Conservative
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